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(54) Title: REGULATION OF HUMAN ELONGASE HSELO1-LIKE PROTEIN

(57) Abstract: Reagents that regulate human elongase HSELO1-like protein and reagents which bind to human elongase HSELO1-like gene products can play a role in preventing, ameliorating, or correcting dysfunctions or diseases including, but not limited to, cancer, diabetes, and CNS disorders.

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REGULATION OF HUMAN ELONGASE HSELO1-LIKE PROTEIN

This application incorporates by reference co-pending provisional applications Serial No. 60/267,150 filed February 8, 2001, Serial No. 60/331,450 filed November 16, 2001, and Serial No. 60/336,164 filed December 6, 2001.

TECHNICAL FIELD OF THE INVENTION

The invention relates to the regulation of human elongase HSELO1-like protein.

BACKGROUND OF THE INVENTION

Elongation enzymes are important in long chain fatty acid synthesis. There is a need in the art to identify related enzymes, which can be regulated to provide therapeutic effects.

SUMMARY OF THE INVENTION

It is an object of the invention to provide reagents and methods of regulating a human elongase HSELO1-like protein. This and other objects of the invention are provided by one or more of the embodiments described below.

One embodiment of the invention is a elongase HSELO1-like protein polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 2;

the amino acid sequence shown in SEQ ID NO: 2

amino acid sequences which are at least about 50% identical to the amino acid

sequence shown in SEQ ID NO: 4 and;

the amino acid sequence shown in SEQ ID NO: 4.

Yet another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a elongase HSELO1-like protein polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 2 ;

the amino acid sequence shown in SEQ ID NO: 2

amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 4 and;

the amino acid sequence shown in SEQ ID NO: 4

Binding between the test compound and the elongase HSELO1-like protein polypeptide is detected. A test compound which binds to the elongase HSELO1-like protein polypeptide is thereby identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the activity of the elongase HSELO1-like protein.

Another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a polynucleotide encoding a elongase HSELO1-like protein polypeptide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 5 and;

the nucleotide sequence shown in SEQ ID NO: 5;

Binding of the test compound to the polynucleotide is detected. A test compound which binds to the polynucleotide is identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the amount of the elongase HSELO1-like protein through interacting with the elongase HSELO1-like protein mRNA.

Another embodiment of the invention is a method of screening for agents which regulate extracellular matrix degradation. A test compound is contacted with a elongase HSELO1-like protein polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 2 ;

the amino acid sequence shown in SEQ ID NO: 2;

amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 4 and ;

the amino acid sequence shown in SEQ ID NO: 4;

A elongase HSELO1-like protein activity of the polypeptide is detected. A test compound which increases elongase HSELO1-like protein activity of the polypeptide relative to elongase HSELO1-like protein activity in the absence of the test compound is thereby identified as a potential agent for increasing extracellular matrix degradation. A test compound which decreases elongase HSELO1-like protein activity of the polypeptide relative to elongase HSELO1-like protein activity in the absence of the test compound is thereby identified as a potential agent for decreasing extracellular matrix degradation.

Even another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a elongase HSELO1-like protein product of a polynucleotide which comprises a nucleotide sequence selected from the group consisting of:

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 5 and ;

the nucleotide sequence shown in SEQ ID NO: 5;

Binding of the test compound to the elongase HSELO1-like protein product is detected. A test compound which binds to the elongase HSELO1-like protein product is thereby identified as a potential agent for decreasing extracellular matrix degradation.

Still another embodiment of the invention is a method of reducing extracellular matrix degradation. A cell is contacted with a reagent which specifically binds to a

polynucleotide encoding a elongase HSELO1-like protein polypeptide or the product encoded by the polynucleotide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 5 and;

the nucleotide sequence shown in SEQ ID NO: 5;

Elongase HSELO1-like protein activity in the cell is thereby decreased.

The invention thus provides a human elongase HSELO1-like protein that can be used to identify test compounds that may act, for example, as activators or inhibitors at the enzyme's active site. Human elongase HSELO1-like protein and fragments thereof also are useful in raising specific antibodies that can block the enzyme and effectively reduce its activity.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:1).

Fig. 2 shows the amino acid sequence deduced from the DNA-sequence of Fig.1 (SEQ ID NO:2).

Fig. 3 shows the amino acid sequence of the protein identified by trembl|AK00034|AK00034_1 (SEQ ID NO:3).

Fig. 4 shows the amino acid sequence deduced from the DNA-sequence of Fig. 5 (SEQ ID NO:4).

Fig. 5 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:5).

Fig. 6 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:6).

Fig. 7 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:7).

Fig. 8 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:8).

Fig. 9 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:9).

Fig. 10 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:10).

Fig. 11 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:11).

Fig. 12 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:12).

Fig. 13 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:13).

Fig. 14 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:14).

Fig. 15 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:15).

Fig. 16 shows the DNA-sequence encoding a elongase HSELO1-like protein Polypeptide (SEQ ID NO:16).

Fig. 17 shows the DNA-sequence of a protein identified by trembl|AF170908|AF170908_1 (SEQ ID NO:17).

Fig. 18 shows the amino acid sequence of a protein identified by trembnewl|AL136939|HSM801903_1 (SEQ ID NO:18).

Fig. 19 shows the amino acid sequence of a protein identified by swiss|P25358|GNS1_YEAST (SEQ ID NO:19).

Fig. 20 shows the amino acid sequence (SEQ ID NO:20).

Fig. 21 shows the BLASTP - alignment of 391_protein_modified (SEQ ID NO:4) against trembl|AK000341|AK000341_1 (SEQ ID NO:3).

Fig. 22. shows the BLASTP - alignment of 391_protein_modified (SEQ ID NO:4) against trembl|AF170908|AF170908_1 (SEQ ID NO:17).

Fig. 23 shows the BLASTP - alignment of 391_protein_modified (SEQ ID NO:4) against aageneseq|Y83932|Y83932.

Fig. 24 shows the BLASTP - alignment of 391_protein_modified (SEQ ID NO:4) against tremblnew|AL136939|HSM801903_1 (SEQ ID NO:18).

Fig. 25 shows the BLASTP - alignment of 391_protein_modified (SEQ ID NO:4) against swiss|P25358|GNS1_YEAST (SEQ ID NO:19).

Fig. 26 shows the BLASTP - alignment of 391_protein_modified (SEQ ID NO:4) against swiss|P40319 (SEQ ID NO:20).

Fig. 27 shows the HMMPFAM - alignment of 391_protein_modified (SEQ ID NO:4) against pfam|hmm|GNS1_SUR4.

Fig. 28 shows the TMHMM result.

Fig. 29 shows the Expression of human elongase HSELO1-like protein.

Fig. 30 shows the Relative expression of human elongase HSELO1-like protein.

Fig. 31 BLASTP - alignment of 391_protein_modified against tremblnew|AF277094|AF277094_1

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to an isolated polynucleotide from the group consisting of:

a) a polynucleotide encoding a elongase HSELO1-like protein polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 2 ;
the amino acid sequence shown in SEQ ID NO: 2
amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 4 and ;
the amino acid sequence shown in SEQ ID NO: 4.

b) a polynucleotide comprising the sequence of SEQ ID NOS: 1 or 5;

c) a polynucleotide which hybridizes under stringent conditions to a polynucleotide specified in (a) and (b) and encodes a elongase HSELO1-like protein polypeptide;

d) a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a elongase HSELO1-like protein polypeptide; and

e) a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d) and encodes a elongase HSELO1-like protein polypeptide.

Furthermore, it has been discovered by the present applicant that a novel elongase HSELO1-like protein, paticularly a human elongase HSELO1-like protein, can be used in therapeutic methods to treat cancer, diabetes, CNS disorder, metabolic disease, asthma or COPD. Human elongase HSELO1-like protein comprises the amino acid sequence shown in SEQ ID NO:2 or 4. Coding sequences for human elongase HSELO1-like protein are shown in SEQ ID NOS:1 and 5. These sequences are contained within the longer sequences shown in SEQ ID NOS:6 and 7. The human elongase HSELO1-like protein gene is located on chromosome 6. Related ESTs (SEQ ID NOS:3 and 8-16) are expressed in fetal liver and spleen, nervous tumor, embryo, pooled three normalized libraries (fetal lung NbHL19W, testis NHT,

and B-cell NCI_CGAP_GCB1), fetal brain, and retinoblastoma.

By sequence similarity and PFAM search, human elongase HSELO1-like protein is a human ortholog of mouse SSC2 and belongs GNS1/SUR4 family (GNS1 and SUR4 are the synonymous names for ELO2 and ELO3, respectively, which are believed to function in very long chain fatty acid elongation). The GNS1/SUR4 family of proteins are evolutionary related-integral membrane proteins. Although its exact function has not yet clearly been established, SSC2 is believed to be a long chain polyunsaturated fatty acid elongation enzyme. . Mouse Cig30, Ssc1 and Ssc2 are newly discovered genes. Experimental findings indicate that these proteins are involved in synthesis of very long chain fatty acids and sphingolipid. Alignments are provided in FIGS. 1-7.

Human elongase HSELO1-like protein is believed to be useful in therapeutic methods to treat disorders such as diabetes, cancer, and CNS disorders. Human elongase HSELO1-like protein also can be used to screen for human elongase HSELO1-like protein activators and inhibitors.

Polypeptides

Human elongase HSELO1-like polypeptides according to the invention comprise at least 6, 10, 15, 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, or 296 contiguous amino acids selected from the amino acid sequence shown in SEQ ID NO:2 or 4 or a biologically active variant thereof, as defined below. An elongase HSELO1-like polypeptide of the invention therefore can be a portion of an elongase HSELO1-like protein, a full-length elongase HSELO1-like protein, or a fusion protein comprising all or a portion of an elongase HSELO1-like protein.

Biologically Active Variants

Human elongase HSELO1-like polypeptide variants which are biologically active,

e.g., retain enzymatic activity, also are human elongase HSELO1-like polypeptides. Preferably, naturally or non-naturally occurring human elongase HSELO1-like polypeptide variants have amino acid sequences which are at least about 50, 55, 60, 65, or 70, preferably about 75, 80, 85, 90, 96, 96, 98, or 99% identical to the amino acid sequence shown in SEQ ID NO:2 or 4 or a fragment thereof. Percent identity between a putative human elongase HSELO1-like polypeptide variant and an amino acid sequence of SEQ ID NO:2 or 4 is determined by conventional methods. See, for example, Altschul *et al.*, *Bull. Math. Bio. 48*:603 (1986), and Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA 89*:10915 (1992). Briefly, two amino acid sequences are aligned to optimize the alignment scores using a gap opening penalty of 10, a gap extension penalty of 1, and the "BLOSUM62" scoring matrix of Henikoff & Henikoff, 1992.

Those skilled in the art appreciate that there are many established algorithms available to align two amino acid sequences. The "FASTA" similarity search algorithm of Pearson & Lipman is a suitable protein alignment method for examining the level of identity shared by an amino acid sequence disclosed herein and the amino acid sequence of a putative variant. The FASTA algorithm is described by Pearson & Lipman, *Proc. Nat'l Acad. Sci. USA 85*:2444(1988), and by Pearson, *Meth. Enzymol. 183*:63 (1990). Briefly, FASTA first characterizes sequence similarity by identifying regions shared by the query sequence (*e.g.*, SEQ ID NO: 2 or 4) and a test sequence that have either the highest density of identities (if the ktup variable is 1) or pairs of identities (if ktup=2), without considering conservative amino acid substitutions, insertions, or deletions. The ten regions with the highest density of identities are then rescored by comparing the similarity of all paired amino acids using an amino acid substitution matrix, and the ends of the regions are "trimmed" to include only those residues that contribute to the highest score. If there are several regions with scores greater than the "cutoff" value (calculated by a predetermined formula based upon the length of the sequence the ktup value), then the trimmed initial regions are examined to determine whether the regions can be joined to form an approximate alignment with gaps. Finally, the highest scoring regions of the two

amino acid sequences are aligned using a modification of the Needleman-Wunsch-Sellers algorithm (Needleman & Wunsch, *J. Mol. Biol.48*:444 (1970); Sellers, *SIAM J. Appl. Math.26*:787 (1974)), which allows for amino acid insertions and deletions. Preferred parameters for FASTA analysis are: ktup=1, gap opening penalty=10, gap extension penalty=1, and substitution matrix=BLOSUM62. These parameters can be introduced into a FASTA program by modifying the scoring matrix file ("SMATRIX"), as explained in Appendix 2 of Pearson, *Meth. Enzymol. 183*:63 (1990).

FASTA can also be used to determine the sequence identity of nucleic acid molecules using a ratio as disclosed above. For nucleotide sequence comparisons, the ktup value can range between one to six, preferably from three to six, most preferably three, with other parameters set as default.

Variations in percent identity can be due, for example, to amino acid substitutions, insertions, or deletions. Amino acid substitutions are defined as one for one amino acid replacements. They are conservative in nature when the substituted amino acid has similar structural and/or chemical properties. Examples of conservative replacements are substitution of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine.

Amino acid insertions or deletions are changes to or within an amino acid sequence. They typically fall in the range of about 1 to 5 amino acids. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological or immunological activity of a human elongase HSELO1-like polypeptide can be found using computer programs well known in the art, such as DNASTAR software.

The invention additionally, encompasses elongase HSELO1-like polypeptides that are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking

groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications can be carried out by known techniques including, but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, $NaBH_4$, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

Additional post-translational modifications encompassed by the invention include, for example, *e.g.*, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. The elongase HSELO1-like polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

The invention also provides chemically modified derivatives of elongase HSELO1-like polypeptides that may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization can be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol, and the like. The polypeptides can be modified at random or predetermined positions within the molecule and can include one, two, three, or more attached chemical moieties.

Whether an amino acid change or a polypeptide modification results in a biologically active elongase HSELO1-like polypeptide can readily be determined by assaying for enzymatic activity, as described for example, in Ghioni *et al.*, Biochim Biophys Acta 1999 Feb 25;1437(2):170-81; Tocher, Lipids 1993 Apr;28(4):267-72; or Chang *et al.*, J Nutr 1992 Nov;122(11):2074-80.

Fusion Proteins

Fusion proteins are useful for generating antibodies against elongase HSELO1-like polypeptide amino acid sequences and for use in various assay systems. For example, fusion proteins can be used to identify proteins that interact with portions of an elongase HSELO1-like polypeptide. Protein affinity chromatography or library-based assays for protein-protein interactions, such as the yeast two-hybrid or phage display systems, can be used for this purpose. Such methods are well known in the art and also can be used as drug screens.

An elongase HSELO1-like polypeptide fusion protein comprises two polypeptide segments fused together by means of a peptide bond. The first polypeptide segment comprises at least 6, 10, 15, 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, or 296 contiguous amino acids of SEQ ID NO:2 or of a biologically active variant, such as those described above. The first polypeptide segment also can comprise full-length elongase HSELO1-like protein.

The second polypeptide segment can be a full-length protein or a protein fragment. Proteins commonly used in fusion protein construction include β-galactosidase, β-glucuronidase, green fluorescent protein (GFP), autofluorescent proteins, including blue fluorescent protein (BFP), glutathione-S-transferase (GST), luciferase, horseradish peroxidase (HRP), and chloramphenicol acetyltransferase (CAT). Additionally, epitope tags are used in fusion protein constructions, including histidine (His) tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Other fusion constructions can include maltose binding protein (MBP), S-tag, Lex a DNA binding domain (DBD) fusions, GAL4 DNA binding domain fusions, and herpes simplex virus (HSV) BP16 protein fusions. A fusion protein also can be engineered to contain a cleavage site located between the elongase HSELO1-like polypeptide-encoding sequence and the heterologous protein sequence, so that the elongase HSELO1-like polypeptide can be cleaved and purified away from the heterologous moiety.

A fusion protein can be synthesized chemically, as is known in the art. Preferably, a fusion protein is produced by covalently linking two polypeptide segments or by standard procedures in the art of molecular biology. Recombinant DNA methods can be used to prepare fusion proteins, for example, by making a DNA construct which comprises coding sequences selected from SEQ ID NO:1 or 5 in proper reading frame with nucleotides encoding the second polypeptide segment and expressing the DNA construct in a host cell, as is known in the art. Many kits for constructing fusion proteins are available from companies such as Promega Corporation (Madison, WI), Stratagene (La Jolla, CA), CLONTECH (Mountain View, CA), Santa Cruz Biotechnology (Santa Cruz, CA), MBL International Corporation (MIC; Watertown, MA), and Quantum Biotechnologies (Montreal, Canada; 1-888-DNA-KITS).

Identification of Species Homologs

Species homologs of human elongase HSELO1-like polypeptide can be obtained using elongase HSELO1-like polypeptide polynucleotides (described below) to make suitable probes or primers for screening cDNA expression libraries from other species, such as mice, monkeys, or yeast, identifying cDNAs which encode homologs of elongase HSELO1-like polypeptide, and expressing the cDNAs as is known in the art.

Polynucleotides

An elongase HSELO1-like polynucleotide can be single- or double-stranded and comprises a coding sequence or the complement of a coding sequence for an elongase HSELO1-like polypeptide. Coding sequences for human elongase HSELO1-like protein are shown in SEQ ID NOS:1 and 5.

Degenerate nucleotide sequences encoding human elongase HSELO1-like polypeptides, as well as homologous nucleotide sequences which are at least about 50, 55, 60, 65, 70, preferably about 75, 90, 96, 98, or 99% identical to the nucleotide sequence shown in SEQ ID NO:1 or 5 or their complements also are elongase HSELO1-like polynucleotides. Percent sequence identity between the sequences of two polynucleotides is determined using computer programs such as ALIGN which employ the FASTA algorithm, using an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2. Complementary DNA (cDNA) molecules, species homologs, and variants of elongase HSELO1-like polynucleotides that encode biologically active elongase HSELO1-like polypeptides also are elongase HSELO1-like polynucleotides. Polynucleotide fragments comprising at least 8, 9, 10, 11, 12, 15, 20, or 25 contiguous nucleotides of SEQ ID NO:1 or 5 or the complement thereof also are elongase HSELO1-like polynucleotides. These fragments can be used, for example, as hybridization probes or as antisense oligonucleotides.

Identification of Polynucleotide Variants and Homologs

Variants and homologs of the elongase HSELO1-like polynucleotides described above also are elongase HSELO1-like polynucleotides. Typically, homologous elongase HSELO1-like polynucleotide sequences can be identified by hybridization of candidate polynucleotides to known elongase HSELO1-like polynucleotides under stringent conditions, as is known in the art. For example, using the following wash conditions--2X SSC (0.3 M NaCl, 0.03 M sodium citrate, pH 7.0), 0.1% SDS, room temperature twice, 30 minutes each; then 2X SSC, 0.1% SDS, 50 °C once, 30 minutes; then 2X SSC, room temperature twice, 10 minutes each--homologous sequences can be identified which contain at most about 25-30% basepair mismatches. More preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches.

Species homologs of the elongase HSELO1-like polynucleotides disclosed herein also can be identified by making suitable probes or primers and screening cDNA expression libraries from other species, such as mice, monkeys, or yeast. Human variants of elongase HSELO1-like polynucleotides can be identified, for example, by screening human cDNA expression libraries. It is well known that the T_m of a double-stranded DNA decreases by 1-1.5 °C with every 1% decrease in homology (Bonner *et al.*, *J. Mol. Biol. 81*, 123 (1973). Variants of human elongase HSELO1-like polynucleotides or elongase HSELO1-like polynucleotides of other species can therefore be identified by hybridizing a putative homologous elongase HSELO1-like polynucleotide with a polynucleotide having a nucleotide sequence of SEQ ID NO:1 or 5 or the complement thereof to form a test hybrid. The melting temperature of the test hybrid is compared with the melting temperature of a hybrid comprising polynucleotides having perfectly complementary nucleotide sequences, and the number or percent of basepair mismatches within the test hybrid is calculated.

Nucleotide sequences which hybridize to elongase HSELO1-like polynucleotides or their complements following stringent hybridization and/or wash conditions also are elongase HSELO1-like polynucleotides. Stringent wash conditions are well known and understood in the art and are disclosed, for example, in Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, 2d ed., 1989, at pages 9.50-9.51.

Typically, for stringent hybridization conditions a combination of temperature and salt concentration should be chosen that is approximately 12-20 °C below the calculated T_m of the hybrid under study. The T_m of a hybrid between an elongase HSELO1-like polynucleotide having a nucleotide sequence shown in SEQ ID NO:1 or 5 or the complement thereof and a polynucleotide sequence which is at least about 50, preferably about 75, 90, 96, or 98% identical to one of those nucleotide sequences can be calculated, for example, using the equation of Bolton and McCarthy, *Proc. Natl. Acad. Sci. U.S.A. 48*, 1390 (1962):

$$T_m = 81.5\ ^\circ C - 16.6(\log_{10}[Na^+]) + 0.41(\%G + C) - 0.63(\%\text{formamide}) - 600/l),$$

where l = the length of the hybrid in basepairs.

Stringent wash conditions include, for example, 4X SSC at 65 °C, or 50% formamide, 4X SSC at 42 °C, or 0.5X SSC, 0.1% SDS at 65 °C. Highly stringent wash conditions include, for example, 0.2X SSC at 65 °C.

Preparation of Polynucleotides

An elongase HSELO1-like polynucleotide can be isolated free of other cellular components such as membrane components, proteins, and lipids. Polynucleotides can be made by a cell and isolated using standard nucleic acid purification techniques, or synthesized using an amplification technique, such as the polymerase chain reaction (PCR), or by using an automatic synthesizer. Methods for isolating polynucleotides are routine and are known in the art. Any such technique for obtaining a polynucleotide can be used to obtain isolated elongase HSELO1-like polynucleotides. For example, restriction enzymes and probes can be used to isolate polynucleotide fragments, which comprise elongase HSELO1-like protein nucleotide sequences. Isolated polynucleotides are in preparations that are free or at least 70, 80, or 90% free of other molecules.

Human elongase HSELO1-like cDNA molecules can be made with standard molecular biology techniques, using elongase HSELO1-like mRNA as a template. Human elongase HSELO1-like cDNA molecules can thereafter be replicated using molecular biology techniques known in the art and disclosed in manuals such as Sambrook *et al.* (1989). An amplification technique, such as PCR, can be used to obtain additional copies of polynucleotides of the invention, using either human genomic DNA or cDNA as a template.

Alternatively, synthetic chemistry techniques can be used to synthesize elongase HSELO1-like polynucleotides. The degeneracy of the genetic code allows alternate

nucleotide sequences to be synthesized which will encode an elongase HSELO1-like polypeptide having, for example, an amino acid sequence shown in SEQ ID NO:2 or 4 or a biologically active variant thereof.

Extending Polynucleotides

Various PCR-based methods can be used to extend the nucleic acid sequences disclosed herein to detect upstream sequences such as promoters and regulatory elements. For example, restriction-site PCR uses universal primers to retrieve unknown sequence adjacent to a known locus (Sarkar, *PCR Methods Applic. 2*, 318-322, 1993). Genomic DNA is first amplified in the presence of a primer to a linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR also can be used to amplify or extend sequences using divergent primers based on a known region (Triglia *et al.*, *Nucleic Acids Res. 16*, 8186, 1988). Primers can be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences Inc., Plymouth, Minn.), to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68-72 °C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Another method which can be used is capture PCR, which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom *et al.*, *PCR Methods Applic. 1*, 111-119, 1991). In this method, multiple restriction enzyme digestions and ligations also can

be used to place an engineered double-stranded sequence into an unknown fragment of the DNA molecule before performing PCR.

Another method which can be used to retrieve unknown sequences is that of Parker *et al.*, *Nucleic Acids Res. 19*, 3055-3060, 1991). Additionally, PCR, nested primers, and PROMOTERFINDER libraries (CLONTECH, Palo Alto, Calif.) can be used to walk genomic DNA (CLONTECH, Palo Alto, Calif.). This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Randomly-primed libraries are preferable, in that they will contain more sequences which contain the 5' regions of genes. Use of a randomly primed library may be especially preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries can be useful for extension of sequence into 5' non-transcribed regulatory regions.

Commercially available capillary electrophoresis systems can be used to analyze the size or confirm the nucleotide sequence of PCR or sequencing products. For example, capillary sequencing can employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) that are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity can be converted to electrical signal using appropriate software (*e.g.* GENOTYPER and Sequence NAVIGATOR, Perkin Elmer), and the entire process from loading of samples to computer analysis and electronic data display can be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA that might be present in limited amounts in a particular sample.

Obtaining Polypeptides

Human elongase HSELO1-like polypeptides can be obtained, for example, by purification from human cells, by expression of elongase HSELO1-like polynucleotides, or by direct chemical synthesis.

Protein Purification

Human elongase HSELO1-like polypeptides can be purified from any cell that expresses the polypeptide, including host cells that have been transfected with elongase HSELO1-like protein expression constructs. A purified elongase HSELO1-like polypeptide is separated from other compounds that normally associate with the elongase HSELO1-like polypeptide in the cell, such as certain proteins, carbohydrates, or lipids, using methods well-known in the art. Such methods include, but are not limited to, size exclusion chromatography, ammonium sulfate fractionation, ion exchange chromatography, affinity chromatography, and preparative gel electrophoresis. A preparation of purified elongase HSELO1-like polypeptides is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure. Purity of the preparations can be assessed by any means known in the art, such as SDS-polyacrylamide gel electrophoresis.

Expression of Polynucleotides

To express an elongase HSELO1-like polynucleotide, the polynucleotide can be inserted into an expression vector that contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods that are well known to those skilled in the art can be used to construct expression vectors containing sequences encoding elongase HSELO1-like polypeptides and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook *et al.*

(1989) and in Ausubel *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, N.Y., 1989.

A variety of expression vector/host systems can be utilized to contain and express sequences encoding an elongase HSELO1-like polypeptide. These include, but are not limited to, microorganisms, such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors, insect cell systems infected with virus expression vectors (*e.g.*, baculovirus), plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids), or animal cell systems.

The control elements or regulatory sequences are those non-translated regions of the vector -- enhancers, promoters, 5' and 3' untranslated regions -- which interact with host cellular proteins to carry out transcription and translation. Such elements can vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, can be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the BLUESCRIPT phagemid (Stratagene, LaJolla, Calif.) or pSPORT1 plasmid (Life Technologies) and the like can be used. The baculovirus polyhedrin promoter can be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (*e.g.*, heat shock, RUBISCO, and storage genes) or from plant viruses (*e.g.*, viral promoters or leader sequences) can be cloned into the vector. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of a nucleotide sequence encoding an elongase HSELO1-like polypeptide, vectors based on SV40 or EBV can be used with an appropriate selectable marker.

Bacterial and Yeast Expression Systems

In bacterial systems, a number of expression vectors can be selected depending upon the use intended for the elongase HSELO1-like polypeptide. For example, when a large quantity of an elongase HSELO1-like polypeptide is needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified can be used. Such vectors include, but are not limited to, multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene). In a BLUESCRIPT vector, a sequence encoding the elongase HSELO1-like polypeptide can be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β-galactosidase so that a hybrid protein is produced. pIN vectors (Van Heeke & Schuster, *J. Biol. Chem. 264*, 5503-5509, 1989) or pGEX vectors (Promega, Madison, Wis.) also can be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems can be designed to include heparin, thrombin, or factor Xa protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH can be used. For reviews, see Ausubel *et al.* (1989) and Grant *et al.*, *Methods Enzymol. 153*, 516-544, 1987.

Plant and Insect Expression Systems

If plant expression vectors are used, the expression of sequences encoding elongase HSELO1-like polypeptides can be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV can be used alone or in combination with the omega leader sequence from TMV (Takamatsu,

EMBO J. 6, 307-311, 1987). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters can be used (Coruzzi *et al.*, *EMBO J. 3*, 1671-1680, 1984; Broglie *et al.*, *Science 224*, 838-843, 1984; Winter *et al.*, *Results Probl. Cell Differ. 17*, 85-105, 1991). These constructs can be introduced into plant cells by direct DNA transformation or by pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (*e.g.*, Hobbs or Murray, in MCGRAW HILL YEARBOOK OF SCIENCE AND TECHNOLOGY, McGraw Hill, New York, N.Y., pp. 191-196, 1992).

An insect system also can be used to express an elongase HSELO1-like polypeptide. For example, in one such system *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. Sequences encoding elongase HSELO1-like polypeptides can be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of elongase HSELO1-like polypeptides will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses can then be used to infect *S. frugiperda cells* or *Trichoplusia* larvae in which elongase HSELO1-like polypeptides can be expressed (Engelhard *et al.*, *Proc. Nat. Acad. Sci. 91*, 3224-3227, 1994).

Mammalian Expression Systems

A number of viral-based expression systems can be used to express elongase HSELO1-like polypeptides in mammalian host cells. For example, if an adenovirus is used as an expression vector, sequences encoding elongase HSELO1-like polypeptides can be ligated into an adenovirus transcription/translation complex comprising the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome can be used to obtain a viable virus that is capable of expressing an elongase HSELO1-like polypeptide in infected host cells (Logan & Shenk, *Proc. Natl. Acad. Sci. 81*, 3655-3659, 1984). If desired,

transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, can be used to increase expression in mammalian host cells.

Human artificial chromosomes (HACs) also can be used to deliver larger fragments of DNA than can be contained and expressed in a plasmid. HACs of 6M to 10M are constructed and delivered to cells via conventional delivery methods (*e.g.*, liposomes, polycationic amino polymers, or vesicles).

Specific initiation signals also can be used to achieve more efficient translation of sequences encoding elongase HSELO1-like polypeptides. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding an elongase HSELO1-like polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals (including the ATG initiation codon) should be provided. The initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used (see Scharf *et al.*, *Results Probl. Cell Differ. 20*, 125-162, 1994).

Host Cells

A host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed elongase HSELO1-like polypeptide in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the polypeptide also can be used to facilitate correct insertion, folding and/or function. Different host cells that have specific cellular machinery and characteristic

mechanisms for post-translational activities (*e.g.*, CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC; 10801 University Boulevard, Manassas, VA 20110-2209) and can be chosen to ensure the correct modification and processing of the foreign protein.

Stable expression is preferred for long-term, high-yield production of recombinant proteins. For example, cell lines which stably express elongase HSELO1-like polypeptides can be transformed using expression vectors which can contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells can be allowed to grow for 1-2 days in an enriched medium before they are switched to a selective medium. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced elongase HSELO1-like protein sequences. Resistant clones of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type. See, for example, ANIMAL CELL CULTURE; R.I. Freshney, ed., 1986.

Any number of selection systems can be used to recover transformed cell lines.

These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler *et al.*, *Cell 11*, 223-32, 1977) and adenine phosphoribosyltransferase (Lowy *et al.*, *Cell 22*, 817-23, 1980) genes which can be employed in *tk*$^-$ or *aprt*$^-$ cells, respectively. Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate (Wigler *et al.*, *Proc. Natl. Acad. Sci. 77*, 3567-70, 1980), *npt* confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin *et al.*, *J. Mol. Biol. 150*, 1-14, 1981), and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murray, 1992, *supra*). Additional selectable genes have been described. For example, *trpB* allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine

(Hartman & Mulligan, *Proc. Natl. Acad. Sci. 85*, 8047-51, 1988). Visible markers such as anthocyanins, β-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, can be used to identify transformants and to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes *et al.*, *Methods Mol. Biol. 55*, 121-131, 1995).

Detecting Expression

Although the presence of marker gene expression suggests that the elongase HSELO1-like polynucleotide is also present, its presence and expression may need to be confirmed. For example, if a sequence encoding an elongase HSELO1-like polypeptide is inserted within a marker gene sequence, transformed cells containing sequences that encode an elongase HSELO1-like polypeptide can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding an elongase HSELO1-like polypeptide under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the elongase HSELO1-like polynucleotide.

Alternatively, host cells which contain an elongase HSELO1-like polynucleotide and which express an elongase HSELO1-like polypeptide can be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques that include membrane, solution, or chip-based technologies for the detection and/or quantification of nucleic acid or protein. For example, the presence of a polynucleotide sequence encoding an elongase HSELO1-like polypeptide can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or fragments or fragments of polynucleotides encoding an elongase HSELO1-like polypeptide. Nucleic acid amplification-based assays involve the use of oligonucleotides selected from sequences encoding an elongase HSELO1-

like polypeptide to detect transformants that contain an elongase HSELO1-like polynucleotide.

A variety of protocols for detecting and measuring the expression of an elongase HSELO1-like polypeptide, using either polyclonal or monoclonal antibodies specific for the polypeptide, are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay using monoclonal antibodies reactive to two non-interfering epitopes on an elongase HSELO1-like polypeptide can be used, or a competitive binding assay can be employed. These and other assays are described in Hampton *et al.*, SEROLOGICAL METHODS: A LABORATORY MANUAL, APS Press, St. Paul, Minn., 1990) and Maddox *et al.*, *J. Exp. Med. 158*, 1211-1216, 1983).

A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding elongase HSELO1-like polypeptides include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, sequences encoding an elongase HSELO1-like polypeptide can be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of labeled nucleotides and an appropriate RNA polymerase such as T7, T3, or SP6. These procedures can be conducted using a variety of commercially available kits (Amersham Pharmacia Biotech, Promega, and US Biochemical). Suitable reporter molecules or labels which can be used for ease of detection include radionuclides, enzymes, and fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Expression and Purification of Polypeptides

Host cells transformed with nucleotide sequences encoding an elongase HSELO1-like polypeptide can be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The polypeptide produced by a transformed cell can be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode elongase HSELO1-like polypeptides can be designed to contain signal sequences which direct secretion of soluble elongase HSELO1-like polypeptides through a prokaryotic or eukaryotic cell membrane or which direct the membrane insertion of membrane-bound elongase HSELO1-like polypeptide.

As discussed above, other constructions can be used to join a sequence encoding an elongase HSELO1-like polypeptide to a nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). Inclusion of cleavable linker sequences such as those specific for Factor Xa or enterokinase (Invitrogen, San Diego, CA) between the purification domain and the elongase HSELO1-like polypeptide also can be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing an elongase HSELO1-like polypeptide and 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification by IMAC (immobilized metal ion affinity chromatography, as described in Porath *et al.*, *Prot. Exp. Purif. 3*, 263-281, 1992), while the enterokinase cleavage site provides a means for purifying the elongase HSELO1-like polypeptide from the fusion protein. Vectors that contain fusion proteins are disclosed in Kroll *et al.*, *DNA Cell Biol. 12*, 441-453, 1993.

Chemical Synthesis

Sequences encoding an elongase HSELO1-like polypeptide can be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers *et al.*, *Nucl. Acids Res. Symp. Ser.* 215-223, 1980; Horn *et al. Nucl. Acids Res. Symp. Ser.* 225-232, 1980). Alternatively, an elongase HSELO1-like polypeptide itself can be produced using chemical methods to synthesize its amino acid sequence, such as by direct peptide synthesis using solid-phase techniques (Merrifield, *J. Am. Chem. Soc. 85*, 2149-2154, 1963; Roberge *et al.*, *Science 269*, 202-204, 1995). Protein synthesis can be performed using manual techniques or by automation. Automated synthesis can be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Optionally, fragments of elongase HSELO1-like polypeptides can be separately synthesized and combined using chemical methods to produce a full-length molecule.

The newly synthesized peptide can be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, PROTEINS: STRUCTURES AND MOLECULAR PRINCIPLES, WH Freeman and Co., New York, N.Y., 1983). The composition of a synthetic elongase HSELO1-like polypeptide can be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure; *see* Creighton, *supra*). Additionally, any portion of the amino acid sequence of the elongase HSELO1-like polypeptide can be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins to produce a variant polypeptide or a fusion protein.

Production of Altered Polypeptides

As will be understood by those of skill in the art, it may be advantageous to produce elongase HSELO1-like polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular

prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce an RNA transcript having desirable properties, such as a half-life that is longer than that of a transcript generated from the naturally occurring sequence.

The nucleotide sequences disclosed herein can be engineered using methods generally known in the art to alter elongase HSELO1-like polypeptide-encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the polypeptide or mRNA product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides can be used to engineer the nucleotide sequences. For example, site-directed mutagenesis can be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth.

Antibodies

Any type of antibody known in the art can be generated to bind specifically to an epitope of an elongase HSELO1-like polypeptide. "Antibody" as used herein includes intact immunoglobulin molecules, as well as fragments thereof, such as Fab, $F(ab')_2$, and Fv, which are capable of binding an epitope of an elongase HSELO1-like polypeptide. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids.

An antibody which specifically binds to an epitope of an elongase HSELO1-like polypeptide can be used therapeutically, as well as in immunochemical assays, such as Western blots, ELISAs, radioimmunoassays, immunohistochemical assays, immunoprecipitations, or other immunochemical assays known in the art. Various immunoassays can be used to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays are well

known in the art. Such immunoassays typically involve the measurement of complex formation between an immunogen and an antibody that specifically binds to the immunogen.

Typically, an antibody which specifically binds to an elongase HSELO1-like polypeptide provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in an immunochemical assay. Preferably, antibodies which specifically bind to elongase HSELO1-like polypeptides do not detect other proteins in immunochemical assays and can immunoprecipitate an elongase HSELO1-like polypeptide from solution.

Human elongase HSELO1-like polypeptides can be used to immunize a mammal, such as a mouse, rat, rabbit, guinea pig, monkey, or human, to produce polyclonal antibodies. If desired, an elongase HSELO1-like polypeptide can be conjugated to a carrier protein, such as bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin. Depending on the host species, various adjuvants can be used to increase the immunological response. Such adjuvants include, but are not limited to, Freund's adjuvant, mineral gels (*e.g.*, aluminum hydroxide), and surface active substances (*e.g.* lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol). Among adjuvants used in humans, BCG (*bacilli Calmette-Guerin*) and *Corynebacterium parvum* are especially useful.

Monoclonal antibodies that specifically bind to an elongase HSELO1-like polypeptide can be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These techniques include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler *et al.*, *Nature 256*, 495-497, 1985; Kozbor *et al.*, *J. Immunol. Methods 81*, 31-42, 1985; Cote *et al.*, *Proc. Natl. Acad. Sci. 80*, 2026-2030, 1983; Cole *et al.*, *Mol. Cell Biol. 62*, 109-120, 1984).

In addition, techniques developed for the production of "chimeric antibodies," the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used (Morrison *et al.*, *Proc. Natl. Acad. Sci. 81*, 6851-6855, 1984; Neuberger *et al.*, *Nature 312*, 604-608, 1984; Takeda *et al.*, *Nature 314*, 452-454, 1985). Monoclonal and other antibodies also can be "humanized" to prevent a patient from mounting an immune response against the antibody when it is used therapeutically. Such antibodies may be sufficiently similar in sequence to human antibodies to be used directly in therapy or may require alteration of a few key residues. Sequence differences between rodent antibodies and human sequences can be minimized by replacing residues which differ from those in the human sequences by site directed mutagenesis of individual residues or by grating of entire complementarity determining regions. Alternatively, humanized antibodies can be produced using recombinant methods, as described in GB2188638B. Antibodies that specifically bind to an elongase HSELO1-like polypeptide can contain antigen binding sites which are either partially or fully humanized, as disclosed in U.S. 5,565,332.

Alternatively, techniques described for the production of single chain antibodies can be adapted using methods known in the art to produce single chain antibodies that specifically bind to elongase HSELO1-like polypeptides. Antibodies with related specificity, but of distinct idiotypic composition, can be generated by chain shuffling from random combinatorial immunoglobin libraries (Burton, *Proc. Natl. Acad. Sci. 88*, 11120-23, 1991).

Single-chain antibodies also can be constructed using a DNA amplification method, such as PCR, using hybridoma cDNA as a template (Thirion *et al.*, 1996, *Eur. J. Cancer Prev. 5*, 507-11). Single-chain antibodies can be mono- or bispecific, and can be bivalent or tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught, for example, in Coloma & Morrison, 1997, *Nat. Biotechnol. 15*, 159-63. Construction of bivalent, bispecific single-chain antibodies is taught in Mallender & Voss, 1994, *J. Biol. Chem. 269*, 199-206.

A nucleotide sequence encoding a single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into an expression construct using standard recombinant DNA methods, and introduced into a cell to express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology (Verhaar *et al.*, 1995, *Int. J. Cancer 61*, 497-501; Nicholls *et al.*, 1993, *J. Immunol. Meth. 165*, 81-91).

Antibodies which specifically bind to elongase HSELO1-like polypeptides also can be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi *et al.*, *Proc. Natl. Acad. Sci. 86*, 3833-3837, 1989; Winter *et al.*, *Nature 349*, 293-299, 1991).

Other types of antibodies can be constructed and used therapeutically in methods of the invention. For example, chimeric antibodies can be constructed as disclosed in WO 93/03151. Binding proteins which are derived from immunoglobulins and which are multivalent and multispecific, such as the "diabodies" described in WO 94/13804, also can be prepared.

Antibodies according to the invention can be purified by methods well known in the art. For example, antibodies can be affinity purified by passage over a column to which an elongase HSELO1-like polypeptide is bound. The bound antibodies can then be eluted from the column using a buffer with a high salt concentration.

Antisense Oligonucleotides

Antisense oligonucleotides are nucleotide sequences that are complementary to a specific DNA or RNA sequence. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form complexes and block either transcription or translation. Preferably, an antisense oligonucleotide

is at least 11 nucleotides in length, but can be at least 12, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides long. Longer sequences also can be used. Antisense oligonucleotide molecules can be provided in a DNA construct and introduced into a cell as described above to decrease the level of elongase HSELO1-like gene products in the cell.

Antisense oligonucleotides can be deoxyribonucleotides, ribonucleotides, or a combination of both. Oligonucleotides can be synthesized manually or by an automated synthesizer, by covalently linking the 5' end of one nucleotide with the 3' end of another nucleotide with non-phosphodiester internucleotide linkages such alkylphosphonates, phosphorothioates, phosphorodithioates, alkylphosphonothioates, alkylphosphonates, phosphoramidates, phosphate esters, carbamates, acetamidate, carboxymethyl esters, carbonates, and phosphate triesters. *See* Brown, *Meth. Mol. Biol. 20*, 1-8, 1994; Sonveaux, *Meth. Mol. Biol. 26*, 1-72, 1994; Uhlmann *et al.*, *Chem. Rev. 90*, 543-583, 1990.

Modifications of elongase HSELO1-like gene expression can be obtained by designing antisense oligonucleotides that will form duplexes to the control, 5', or regulatory regions of the elongase HSELO1-like gene. Oligonucleotides derived from the transcription initiation site, *e.g.*, between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or chaperons. Therapeutic advances using triplex DNA have been described in the literature (*e.g.*, Gee *et al.*, in Huber & Carr, MOLECULAR AND IMMUNOLOGIC APPROACHES, Futura Publishing Co., Mt. Kisco, N.Y., 1994). An antisense oligonucleotide also can be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Precise complementarity is not required for successful complex formation between an antisense oligonucleotide and the complementary sequence of an elongase

HSELO1-like polynucleotide. Antisense oligonucleotides which comprise, for example, 2, 3, 4, or 5 or more stretches of contiguous nucleotides which are precisely complementary to an elongase HSELO1-like polynucleotide, each separated by a stretch of contiguous nucleotides which are not complementary to adjacent elongase HSELO1-like protein nucleotides, can provide sufficient targeting specificity for elongase HSELO1-like mRNA. Preferably, each stretch of complementary contiguous nucleotides is at least 4, 5, 6, 7, or 8 or more nucleotides in length. Non-complementary intervening sequences are preferably 1, 2, 3, or 4 nucleotides in length. One skilled in the art can easily use the calculated melting point of an antisense-sense pair to determine the degree of mismatching which will be tolerated between a particular antisense oligonucleotide and a particular elongase HSELO1-like polynucleotide sequence.

Antisense oligonucleotides can be modified without affecting their ability to hybridize to an elongase HSELO1-like polynucleotide. These modifications can be internal or at one or both ends of the antisense molecule. For example, internucleoside phosphate linkages can be modified by adding cholesteryl or diamine moieties with varying numbers of carbon residues between the amino groups and terminal ribose. Modified bases and/or sugars, such as arabinose instead of ribose, or a 3', 5'-substituted oligonucleotide in which the 3' hydroxyl group or the 5' phosphate group are substituted, also can be employed in a modified antisense oligonucleotide. These modified oligonucleotides can be prepared by methods well known in the art. *See, e.g.*, Agrawal *et al.*, *Trends Biotechnol. 10*, 152-158, 1992; Uhlmann *et al.*, *Chem. Rev. 90*, 543-584, 1990; Uhlmann *et al.*, *Tetrahedron. Lett. 215*, 3539-3542, 1987.

Ribozymes

Ribozymes are RNA molecules with catalytic activity. *See, e.g.*, Cech, *Science 236*, 1532-1539; 1987; Cech, *Ann. Rev. Biochem. 59*, 543-568; 1990, Cech, *Curr. Opin. Struct. Biol. 2*, 605-609; 1992, Couture & Stinchcomb, *Trends Genet. 12*, 510-515,

1996. Ribozymes can be used to inhibit gene function by cleaving an RNA sequence, as is known in the art (*e.g.*, Haseloff *et al.*, U.S. Patent 5,641,673). The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Examples include engineered hammerhead motif ribozyme molecules that can specifically and efficiently catalyze endonucleolytic cleavage of specific nucleotide sequences.

The coding sequence of an elongase HSELO1-like polynucleotide can be used to generate ribozymes that will specifically bind to mRNA transcribed from the elongase HSELO1-like polynucleotide. Methods of designing and constructing ribozymes which can cleave other RNA molecules in trans in a highly sequence specific manner have been developed and described in the art (*see* Haseloff *et al. Nature 334*, 585-591, 1988). For example, the cleavage activity of ribozymes can be targeted to specific RNAs by engineering a discrete "hybridization" region into the ribozyme. The hybridization region contains a sequence complementary to the target RNA and thus specifically hybridizes with the target (see, for example, Gerlach *et al.*, EP 321,201).

Specific ribozyme cleavage sites within an elongase HSELO1-like protein RNA target can be identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target RNA containing the cleavage site can be evaluated for secondary structural features which may render the target inoperable. Suitability of candidate elongase HSELO1-like protein RNA targets also can be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays. Longer complementary sequences can be used to increase the affinity of the hybridization sequence for the target. The hybridizing and cleavage regions of the ribozyme can be integrally related such that upon hybridizing

to the target RNA through the complementary regions, the catalytic region of the ribozyme can cleave the target.

Ribozymes can be introduced into cells as part of a DNA construct. Mechanical methods, such as microinjection, liposome-mediated transfection, electroporation, or calcium phosphate precipitation, can be used to introduce a ribozyme-containing DNA construct into cells in which it is desired to decrease elongase HSELO1-like protein expression. Alternatively, if it is desired that the cells stably retain the DNA construct, the construct can be supplied on a plasmid and maintained as a separate element or integrated into the genome of the cells, as is known in the art. A ribozyme-encoding DNA construct can include transcriptional regulatory elements, such as a promoter element, an enhancer or UAS element, and a transcriptional terminator signal, for controlling transcription of ribozymes in the cells.

As taught in Haseloff *et al.*, U.S. Patent 5,641,673, ribozymes can be engineered so that ribozyme expression will occur in response to factors that induce expression of a target gene. Ribozymes also can be engineered to provide an additional level of regulation, so that destruction of mRNA occurs only when both a ribozyme and a target gene are induced in the cells.

Differentially Expressed Genes

Described herein are methods for the identification of genes whose products interact with human elongase HSELO1-like protein. Such genes may represent genes that are differentially expressed in disorders including, but not limited to, diabetes, cancer, and CNS disorders. Further, such genes may represent genes that are differentially regulated in response to manipulations relevant to the progression or treatment of such diseases. Additionally, such genes may have a temporally modulated expression, increased or decreased at different stages of tissue or organism development. A differentially expressed gene may also have its expression modulated under control versus experimental conditions. In addition, the human

elongase HSELO1-like gene or gene product may itself be tested for differential expression.

The degree to which expression differs in a normal versus a diseased state need only be large enough to be visualized via standard characterization techniques such as differential display techniques. Other such standard characterization techniques by which expression differences may be visualized include but are not limited to, quantitative RT (reverse transcriptase), PCR, and Northern analysis.

Identification of Differentially Expressed Genes

To identify differentially expressed genes total RNA or, preferably, mRNA is isolated from tissues of interest. For example, RNA samples are obtained from tissues of experimental subjects and from corresponding tissues of control subjects. Any RNA isolation technique that does not select against the isolation of mRNA may be utilized for the purification of such RNA samples. See, for example, Ausubel *et al.*, ed., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, Inc. New York, 1987-1993. Large numbers of tissue samples may readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski, U.S. Patent 4,843,155.

Transcripts within the collected RNA samples that represent RNA produced by differentially expressed genes are identified by methods well known to those of skill in the art. They include, for example, differential screening (Tedder *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 85*, 208-12, 1988), subtractive hybridization (Hedrick *et al.*, *Nature 308*, 149-53; Lee *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 88*, 2825, 1984), and, preferably, differential display (Liang & Pardee, *Science 257*, 967-71, 1992; U.S. Patent 5,262,311).

The differential expression information may itself suggest relevant methods for the treatment of disorders involving the human elongase HSELO1-like protein. For

example, treatment may include a modulation of expression of the differentially expressed genes and/or the gene encoding the human elongase HSELO1-like protein. The differential expression information may indicate whether the expression or activity of the differentially expressed gene or gene product or the human elongase HSELO1-like gene or gene product are up-regulated or down-regulated.

Screening Methods

The invention provides assays for screening test compounds that bind to or modulate the activity of an elongase HSELO1-like polypeptide or an elongase HSELO1-like polynucleotide. A test compound preferably binds to an elongase HSELO1-like polypeptide or polynucleotide. More preferably, a test compound decreases or increases enzyme activity by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the test compound.

Test Compounds

Test compounds can be pharmacologic agents already known in the art or can be compounds previously unknown to have any pharmacological activity. The compounds can be naturally occurring or designed in the laboratory. They can be isolated from microorganisms, animals, or plants, and can be produced recombinantly, or synthesized by chemical methods known in the art. If desired, test compounds can be obtained using any of the numerous combinatorial library methods known in the art, including but not limited to, biological libraries, spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer, or small molecule libraries of compounds. *See* Lam, *Anticancer Drug Des. 12*, 145, 1997.

Methods for the synthesis of molecular libraries are well known in the art (*see*, for example, DeWitt *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 90*, 6909, 1993; Erb *et al. Proc. Natl. Acad. Sci. U.S.A. 91*, 11422, 1994; Zuckermann *et al.*, *J. Med. Chem. 37*, 2678, 1994; Cho *et al.*, *Science 261*, 1303, 1993; Carell *et al.*, *Angew. Chem. Int. Ed. Engl. 33*, 2059, 1994; Carell *et al.*, *Angew. Chem. Int. Ed. Engl. 33*, 2061; Gallop *et al.*, *J. Med. Chem. 37*, 1233, 1994). Libraries of compounds can be presented in solution (*see, e.g.*, Houghten, *BioTechniques 13*, 412-421, 1992), or on beads (Lam, *Nature 354*, 82-84, 1991), chips (Fodor, *Nature 364*, 555-556, 1993), bacteria or spores (Ladner, U.S. Patent 5,223,409), plasmids (Cull *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 89*, 1865-1869, 1992), or phage (Scott & Smith, *Science 249*, 386-390, 1990; Devlin, *Science 249*, 404-406, 1990); Cwirla *et al.*, *Proc. Natl. Acad. Sci. 97*, 6378-6382, 1990; Felici, *J. Mol. Biol. 222*, 301-310, 1991; and Ladner, U.S. Patent 5,223,409).

High Throughput Screening

Test compounds can be screened for the ability to bind to elongase HSELO1-like polypeptides or polynucleotides or to affect elongase HSELO1-like protein activity or elongase HSELO1-like gene expression using high throughput screening. Using high throughput screening, many discrete compounds can be tested in parallel so that large numbers of test compounds can be quickly screened. The most widely established techniques utilize 96-well microtiter plates. The wells of the microtiter plates typically require assay volumes that range from 50 to 500 µl. In addition to the plates, many instruments, materials, pipettors, robotics, plate washers, and plate readers are commercially available to fit the 96-well format.

Alternatively, "free format assays," or assays that have no physical barrier between samples, can be used. For example, an assay using pigment cells (melanocytes) in a simple homogeneous assay for combinatorial peptide libraries is described by Jayawickreme *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 19*, 1614-18 (1994). The cells are placed under agarose in petri dishes, then beads that carry combinatorial compounds are placed on the surface of the agarose. The combinatorial compounds are partially

released the compounds from the beads. Active compounds can be visualized as dark pigment areas because, as the compounds diffuse locally into the gel matrix, the active compounds cause the cells to change colors.

Another example of a free format assay is described by Chelsky, "Strategies for Screening Combinatorial Libraries: Novel and Traditional Approaches," reported at the First Annual Conference of The Society for Biomolecular Screening in Philadelphia, Pa. (Nov. 7-10, 1995). Chelsky placed a simple homogenous enzyme assay for carbonic anhydrase inside an agarose gel such that the enzyme in the gel would cause a color change throughout the gel. Thereafter, beads carrying combinatorial compounds via a photolinker were placed inside the gel and the compounds were partially released by UV-light. Compounds that inhibited the enzyme were observed as local zones of inhibition having less color change.

Yet another example is described by Salmon *et al.*, *Molecular Diversity 2*, 57-63 (1996). In this example, combinatorial libraries were screened for compounds that had cytotoxic effects on cancer cells growing in agar.

Another high throughput screening method is described in Beutel *et al.*, U.S. Patent 5,976,813. In this method, test samples are placed in a porous matrix. One or more assay components are then placed within, on top of, or at the bottom of a matrix such as a gel, a plastic sheet, a filter, or other form of easily manipulated solid support. When samples are introduced to the porous matrix they diffuse sufficiently slowly, such that the assays can be performed without the test samples running together.

Binding Assays

For binding assays, the test compound is preferably a small molecule that binds to and occupies, for example, the active site of the elongase HSELO1-like polypeptide, such that normal biological activity is prevented. Examples of such small molecules include, but are not limited to, small peptides or peptide-like molecules.

In binding assays, either the test compound or the elongase HSELO1-like polypeptide can comprise a detectable label, such as a fluorescent, radioisotopic, chemiluminescent, or enzymatic label, such as horseradish peroxidase, alkaline phosphatase, or luciferase. Detection of a test compound that is bound to the elongase HSELO1-like polypeptide can then be accomplished, for example, by direct counting of radioemmission, by scintillation counting, or by determining conversion of an appropriate substrate to a detectable product.

Alternatively, binding of a test compound to an elongase HSELO1-like polypeptide can be determined without labeling either of the interactants. For example, a microphysiometer can be used to detect binding of a test compound with an elongase HSELO1-like polypeptide. A microphysiometer (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between a test compound and an elongase HSELO1-like polypeptide (McConnell *et al.*, *Science 257*, 1906-1912, 1992).

Determining the ability of a test compound to bind to an elongase HSELO1-like polypeptide also can be accomplished using a technology such as real-time Bimolecular Interaction Analysis (BIA) (Sjolander & Urbaniczky, *Anal. Chem. 63*, 2338-2345, 1991, and Szabo *et al.*, *Curr. Opin. Struct. Biol. 5*, 699-705, 1995). BIA is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore™). Changes in the optical phenomenon surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

In yet another aspect of the invention, an elongase HSELO1-like polypeptide can be used as a "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent 5,283,317; Zervos *et al.*, *Cell 72*, 223-232, 1993; Madura *et al.*, *J. Biol. Chem.*

268, 12046-12054, 1993; Bartel *et al.*, *BioTechniques 14*, 920-924, 1993; Iwabuchi *et al.*, *Oncogene 8*, 1693-1696, 1993; and Brent W094/10300), to identify other proteins which bind to or interact with the elongase HSELO1-like polypeptide and modulate its activity.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. For example, in one construct, polynucleotide encoding an elongase HSELO1-like polypeptide can be fused to a polynucleotide encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct a DNA sequence that encodes an unidentified protein ("prey" or "sample") can be fused to a polynucleotide that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact *in vivo* to form an protein-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ), which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional transcription factor can be isolated and used to obtain the DNA sequence encoding the protein that interacts with the elongase HSELO1-like polypeptide.

It may be desirable to immobilize either the elongase HSELO1-like polypeptide (or polynucleotide) or the test compound to facilitate separation of bound from unbound forms of one or both of the interactants, as well as to accommodate automation of the assay. Thus, either the elongase HSELO1-like polypeptide (or polynucleotide) or the test compound can be bound to a solid support. Suitable solid supports include, but are not limited to, glass or plastic slides, tissue culture plates, microtiter wells, tubes, silicon chips, or particles such as beads (including, but not limited to, latex, polystyrene, or glass beads). Any method known in the art can be used to attach the enzyme polypeptide (or polynucleotide) or test compound to a solid support, including use of covalent and non-covalent linkages, passive absorption, or pairs of

binding moieties attached respectively to the polypeptide (or polynucleotide) or test compound and the solid support. Test compounds are preferably bound to the solid support in an array, so that the location of individual test compounds can be tracked. Binding of a test compound to an elongase HSELO1-like polypeptide (or polynucleotide) can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and microcentrifuge tubes.

In one embodiment, the elongase HSELO1-like polypeptide is a fusion protein comprising a domain that allows the elongase HSELO1-like polypeptide to be bound to a solid support. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and the non-adsorbed elongase HSELO1-like polypeptide; the mixture is then incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components. Binding of the interactants can be determined either directly or indirectly, as described above. Alternatively, the complexes can be dissociated from the solid support before binding is determined.

Other techniques for immobilizing proteins or polynucleotides on a solid support also can be used in the screening assays of the invention. For example, either an elongase HSELO1-like polypeptide (or polynucleotide) or a test compound can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated elongase HSELO1-like polypeptides (or polynucleotides) or test compounds can be prepared from biotin-NHS(N-hydroxysuccinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.) and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies which specifically bind to an elongase HSELO1-like polypeptide, polynucleotide, or a test compound, but which do not interfere with a desired binding site, such as the

active site of the elongase HSELO1-like polypeptide, can be derivatized to the wells of the plate. Unbound target or protein can be trapped in the wells by antibody conjugation.

Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies which specifically bind to the elongase HSELO1-like polypeptide or test compound, enzyme-linked assays which rely on detecting an activity of the elongase HSELO1-like polypeptide, and SDS gel electrophoresis under non-reducing conditions.

Screening for test compounds which bind to an elongase HSELO1-like polypeptide or polynucleotide also can be carried out in an intact cell. Any cell which comprises an elongase HSELO1-like polypeptide or polynucleotide can be used in a cell-based assay system. An elongase HSELO1-like polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Binding of the test compound to an elongase HSELO1-like polypeptide or polynucleotide is determined as described above.

Enzyme Assays

Test compounds can be tested for the ability to increase or decrease the enzyme activity of a human elongase HSELO1-like polypeptide. Enzyme activity can be measured, for example, as described in Ghioni *et al.*, Biochim Biophys Acta 1999 Feb 25;1437(2):170-81; Tocher, Lipids 1993 Apr;28(4):267-72; or Chang *et al.*, J Nutr 1992 Nov;122(11):2074-80.

Enzyme assays can be carried out after contacting either a purified elongase HSELO1-like polypeptide, a cell membrane preparation, or an intact cell with a test compound. A test compound that decreases an elongase activity of an elongase HSELO1-like polypeptide by at least about 10, preferably about 50, more preferably

about 75, 90, or 100% is identified as a potential therapeutic agent for decreasing elongase HSELO1-like protein activity. A test compound which increases a n elongase activity of a human elongase HSELO1-like polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential therapeutic agent for increasing human elongase HSELO1-like protein activity.

Gene Expression

In another embodiment, test compounds that increase or decrease elongase HSELO1-like gene expression are identified. An elongase HSELO1-like polynucleotide is contacted with a test compound, and the expression of an RNA or polypeptide product of the elongase HSELO1-like polynucleotide is determined. The level of expression of appropriate mRNA or polypeptide in the presence of the test compound is compared to the level of expression of mRNA or polypeptide in the absence of the test compound. The test compound can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater in the presence of the test compound than in its absence, the test compound is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less in the presence of the test compound than in its absence, the test compound is identified as an inhibitor of the mRNA or polypeptide expression.

The level of elongase HSELO1-like mRNA or polypeptide expression in the cells can be determined by methods well known in the art for detecting mRNA or polypeptide. Either qualitative or quantitative methods can be used. The presence of polypeptide products of an elongase HSELO1-like polynucleotide can be determined, for example, using a variety of techniques known in the art, including immunochemical methods such as radioimmunoassay, Western blotting, and immunohistochemistry. Alternatively, polypeptide synthesis can be determined *in vivo*, in a cell culture, or in

an *in vitro* translation system by detecting incorporation of labeled amino acids into an elongase HSELO1-like polypeptide.

Such screening can be carried out either in a cell-free assay system or in an intact cell. Any cell that expresses an elongase HSELO1-like polynucleotide can be used in a cell-based assay system. The elongase HSELO1-like polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Either a primary culture or an established cell line, such as CHO or human embryonic kidney 293 cells, can be used.

Pharmaceutical Compositions

The invention also provides pharmaceutical compositions that can be administered to a patient to achieve a therapeutic effect. Pharmaceutical compositions of the invention can comprise, for example, an elongase HSELO1-like polypeptide, elongase HSELO1-like polynucleotide, ribozymes or antisense oligonucleotides, antibodies which specifically bind to an elongase HSELO1-like polypeptide, or mimetics, activators, or inhibitors of an elongase HSELO1-like polypeptide activity. The compositions can be administered alone or in combination with at least one other agent, such as stabilizing compound, which can be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions can be administered to a patient alone, or in combination with other agents, drugs or hormones.

In addition to the active ingredients, these pharmaceutical compositions can contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries that facilitate processing of the active compounds into preparations which can be used pharmaceutically. Pharmaceutical compositions of the invention can be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, parenteral, topical, sublingual, or rectal

means. Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents can be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores can be used in conjunction with suitable coatings, such as concentrated sugar solutions, which also can contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments can be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, *i.e.*, dosage.

Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds can be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration can be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions can contain substances that increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds can be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Non-lipid polycationic amino polymers also can be used for delivery. Optionally, the suspension also can contain suitable stabilizers or agents that increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention can be manufactured in a manner that is known in the art, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes. The pharmaceutical composition can be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation can be a lyophilized powder which can contain any or all of the following: 1-50 mM histidine, 0.1%-2% sucrose, and 2-7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

Further details on techniques for formulation and administration can be found in the latest edition of REMINGTON'S PHARMACEUTICAL SCIENCES (Maack Publishing Co., Easton, Pa.). After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated

condition. Such labeling would include amount, frequency, and method of administration.

Therapeutic Indications and Methods

Human elongase HSELO1-like protein can be regulated to treat diabetes, cancer, and CNS disorders.

Diabetes.

Diabetes mellitus is a common metabolic disorder characterized by an abnormal elevation in blood glucose, alterations in lipids and abnormalities (complications) in the cardiovascular system, eye, kidney and nervous system. Diabetes is divided into two separate diseases: type 1 diabetes (juvenile onset), which results from a loss of cells which make and secrete insulin, and type 2 diabetes (adult onset), which is caused by a defect in insulin secretion and a defect in insulin action.

Type 1 diabetes is initiated by an autoimuune reaction that attacks the insulin secreting cells (beta cells) in the pancreatic islets. Agents that prevent this reaction from occurring or that stop the reaction before destruction of the beta cells has been accomplished are potential therapies for this disease. Other agents that induce beta cell proliferation and regeneration also are potential therapies.

Type II diabetes is the most common of the two diabetic conditions (6% of the population). The defect in insulin secretion is an important cause of the diabetic condition and results from an inability of the beta cell to properly detect and respond to rises in blood glucose levels with insulin release. Therapies that increase the response by the beta cell to glucose would offer an important new treatment for this disease.

The defect in insulin action in Type II diabetic subjects is another target for therapeutic intervention. Agents that increase the activity of the insulin receptor in muscle, liver, and fat will cause a decrease in blood glucose and a normalization of plasma lipids. The receptor activity can be increased by agents that directly stimulate the receptor or that increase the intracellular signals from the receptor. Other therapies can directly activate the cellular end process, *i.e.* glucose transport or various enzyme systems, to generate an insulin-like effect and therefore a produce beneficial outcome. Because overweight subjects have a greater susceptibility to Type II diabetes, any agent that reduces body weight is a possible therapy.

Both Type I and Type diabetes can be treated with agents that mimic insulin action or that treat diabetic complications by reducing blood glucose levels. Likewise, agents that reduces new blood vessel growth can be used to treat the eye complications that develop in both diseases.

Cancer.

Cancer is a disease fundamentally caused by oncogenic cellular transformation. There are several hallmarks of transformed cells that distinguish them from their normal counterparts and underlie the pathophysiology of cancer. These include uncontrolled cellular proliferation, unresponsiveness to normal death-inducing signals (immortalization), increased cellular motility and invasiveness, increased ability to recruit blood supply through induction of new blood vessel formation (angiogenesis), genetic instability, and dysregulated gene expression. Various combinations of these aberrant physiologies, along with the acquisition of drug-resistance frequently lead to an intractable disease state in which organ failure and patient death ultimately ensue.

Most standard cancer therapies target cellular proliferation and rely on the differential proliferative capacities between transformed and normal cells for their efficacy. This approach is hindered by the facts that several important normal cell types are also

highly proliferative and that cancer cells frequently become resistant to these agents. Thus, the therapeutic indices for traditional anti-cancer therapies rarely exceed 2.0.

The advent of genomics-driven molecular target identification has opened up the possibility of identifying new cancer-specific targets for therapeutic intervention that will provide safer, more effective treatments for cancer patients. Thus, newly discovered tumor-associated genes and their products can be tested for their role(s) in disease and used as tools to discover and develop innovative therapies. Genes playing important roles in any of the physiological processes outlined above can be characterized as cancer targets.

Genes or gene fragments identified through genomics can readily be expressed in one or more heterologous expression systems to produce functional recombinant proteins. These proteins are characterized *in vitro* for their biochemical properties and then used as tools in high-throughput molecular screening programs to identify chemical modulators of their biochemical activities. Agonists and/or antagonists of target protein activity can be identified in this manner and subsequently tested in cellular and *in vivo* disease models for anti-cancer activity. Optimization of lead compounds with iterative testing in biological models and detailed pharmacokinetic and toxicological analyses form the basis for drug development and subsequent testing in humans.

CNS disorders.

CNS disorders which may be treated include brain injuries, cerebrovascular diseases and their consequences, Parkinson's disease, corticobasal degeneration, motor neuron disease, dementia, including ALS, multiple sclerosis, traumatic brain injury, stroke, post-stroke, post-traumatic brain injury, and small-vessel cerebrovascular disease. Dementias, such as Alzheimer's disease, vascular dementia, dementia with Lewy bodies, frontotemporal dementia and Parkinsonism linked to chromosome 17, frontotemporal dementias, including Pick's disease, progressive nuclear palsy,

corticobasal degeneration, Huntington's disease, thalamic degeneration, Creutzfeld-Jakob dementia, HIV dementia, schizophrenia with dementia, and Korsakoff's psychosis also can be treated. Similarly, it may be possible to treat cognitive-related disorders, such as mild cognitive impairment, age-associated memory impairment, age-related cognitive decline, vascular cognitive impairment, attention deficit disorders, attention deficit hyperactivity disorders, and memory disturbances in children with learning disabilities, by regulating the activity of human elongase HSELO1-like protein.

Pain that is associated with CNS disorders also can be treated by regulating the activity of human elongase HSELO1-like protein. Pain which can be treated includes that associated with central nervous system disorders, such as multiple sclerosis, spinal cord injury, sciatica, failed back surgery syndrome, traumatic brain injury, epilepsy, Parkinson's disease, post-stroke, and vascular lesions in the brain and spinal cord (*e.g.*, infarct, hemorrhage, vascular malformation). Non-central neuropathic pain includes that associated with post mastectomy pain, reflex sympathetic dystrophy (RSD), trigeminal neuralgiaradioculopathy, post-surgical pain, HIV/AIDS related pain, cancer pain, metabolic neuropathies (*e.g.*, diabetic neuropathy, vasculitic neuropathy secondary to connective tissue disease), paraneoplastic polyneuropathy associated, for example, with carcinoma of lung, or leukemia, or lymphoma, or carcinoma of prostate, colon or stomach, trigeminal neuralgia, cranial neuralgias, and post-herpetic neuralgia. Pain associated with cancer and cancer treatment also can be treated, as can headache pain (for example, migraine with aura, migraine without aura, and other migraine disorders), episodic and chronic tension-type headache, tension-type like headache, cluster headache, and chronic paroxysmal hemicrania.

This invention further pertains to the use of novel agents identified by the screening assays described above. Accordingly, it is within the scope of this invention to use a test compound identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a modulating agent, an

antisense nucleic acid molecule, a specific antibody, ribozyme, or an elongase HSELO1-like polypeptide binding molecule) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

A reagent which affects elongase HSELO1-like protein activity can be administered to a human cell, either *in vitro* or *in vivo*, to reduce elongase HSELO1-like protein activity. The reagent preferably binds to an expression product of a human elongase HSELO1-like gene. If the expression product is a protein, the reagent is preferably an antibody. For treatment of human cells *ex vivo*, an antibody can be added to a preparation of stem cells that have been removed from the body. The cells can then be replaced in the same or another human body, with or without clonal propagation, as is known in the art.

In one embodiment, the reagent is delivered using a liposome. Preferably, the liposome is stable in the animal into which it has been administered for at least about 30 minutes, more preferably for at least about 1 hour, and even more preferably for at least about 24 hours. A liposome comprises a lipid composition that is capable of targeting a reagent, particularly a polynucleotide, to a particular site in an animal, such as a human. Preferably, the lipid composition of the liposome is capable of targeting to a specific organ of an animal, such as the lung, liver, spleen, heart brain, lymph nodes, and skin.

A liposome useful in the present invention comprises a lipid composition that is capable of fusing with the plasma membrane of the targeted cell to deliver its contents to the cell. Preferably, the transfection efficiency of a liposome is about 0.5 μg of DNA per 16 nmole of liposome delivered to about 10^6 cells, more preferably about 1.0 μg of DNA per 16 nmole of liposome delivered to about 10^6 cells, and even

more preferably about 2.0 μg of DNA per 16 nmol of liposome delivered to about 10^6 cells. Preferably, a liposome is between about 100 and 500 nm, more preferably between about 150 and 450 nm, and even more preferably between about 200 and 400 nm in diameter.

Suitable liposomes for use in the present invention include those liposomes standardly used in, for example, gene delivery methods known to those of skill in the art. More preferred liposomes include liposomes having a polycationic lipid composition and/or liposomes having a cholesterol backbone conjugated to polyethylene glycol. Optionally, a liposome comprises a compound capable of targeting the liposome to a particular cell type, such as a cell-specific ligand exposed on the outer surface of the liposome.

Complexing a liposome with a reagent such as an antisense oligonucleotide or ribozyme can be achieved using methods that are standard in the art (see, for example, U.S. Patent 5,705,151). Preferably, from about 0.1 μg to about 10 μg of polynucleotide is combined with about 8 nmol of liposomes, more preferably from about 0.5 μg to about 5 μg of polynucleotides are combined with about 8 nmol liposomes, and even more preferably about 1.0 μg of polynucleotides is combined with about 8 nmol liposomes.

In another embodiment, antibodies can be delivered to specific tissues *in vivo* using receptor-mediated targeted delivery. Receptor-mediated DNA delivery techniques are taught in, for example, Findeis *et al. Trends in Biotechnol. 11*, 202-05 (1993); Chiou *et al.*, GENE THERAPEUTICS: METHODS AND APPLICATIONS OF DIRECT GENE TRANSFER (J.A. Wolff, ed.) (1994); Wu & Wu, *J. Biol. Chem. 263*, 621-24 (1988); Wu *et al.*, *J. Biol. Chem. 269*, 542-46 (1994); Zenke *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 87*, 3655-59 (1990); Wu *et al.*, *J. Biol. Chem. 266*, 338-42 (1991).

Determination of a Therapeutically Effective Dose

The determination of a therapeutically effective dose is well within the capability of those skilled in the art. A therapeutically effective dose refers to that amount of active ingredient which increases or decreases elongase HSELO1-like protein activity relative to the elongase HSELO1-like protein activity which occurs in the absence of the therapeutically effective dose.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models, usually mice, rabbits, dogs, or pigs. The animal model also can be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

Therapeutic efficacy and toxicity, *e.g.*, ED_{50} (the dose therapeutically effective in 50% of the population) and LD_{50} (the dose lethal to 50% of the population), can be determined by standard pharmaceutical procedures in cell cultures or experimental animals. The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the ratio, LD_{50}/ED_{50}.

Pharmaceutical compositions that exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires treatment. Dosage and administration are adjusted to provide sufficient levels of the active ingredient or to maintain the desired effect. Factors that can be taken into account include the severity of the disease state,

general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions can be administered every 3 to 4 days, every week, or once every two weeks depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts can vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

If the reagent is a single-chain antibody, polynucleotides encoding the antibody can be constructed and introduced into a cell either *ex vivo* or *in vivo* using well-established techniques including, but not limited to, transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, "gene gun," and DEAE- or calcium phosphate-mediated transfection.

Effective *in vivo* dosages of an antibody are in the range of about 5 µg to about 50 µg/kg, about 50 µg to about 5 mg/kg, about 100 µg to about 500 µg/kg of patient body weight, and about 200 to about 250 µg/kg of patient body weight. For administration of polynucleotides encoding single-chain antibodies, effective *in vivo* dosages are in the range of about 100 ng to about 200 ng, 500 ng to about 50 mg, about 1 µg to about 2 mg, about 5 µg to about 500 µg, and about 20 µg to about 100 µg of DNA.

If the expression product is mRNA, the reagent is preferably an antisense oligonucleotide or a ribozyme. Polynucleotides that express antisense oligonucleotides or ribozymes can be introduced into cells by a variety of methods, as described above.

Preferably, a reagent reduces expression of an elongase HSELO1-like gene or the activity of an elongase HSELO1-like polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the reagent. The effectiveness of the mechanism chosen to decrease the level of expression of an elongase HSELO1-like gene or the activity of an elongase HSELO1-like polypeptide can be assessed using methods well known in the art, such as hybridization of nucleotide probes to elongase HSELO1-like protein-specific mRNA, quantitative RT-PCR, immunologic detection of an elongase HSELO1-like polypeptide, or measurement of elongase HSELO1-like protein activity.

In any of the embodiments described above, any of the pharmaceutical compositions of the invention can be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy can be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents can act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

Any of the therapeutic methods described above can be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

Diagnostic Methods

Human elongase HSELO1-like protein also can be used in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic acid sequences that encode the enzyme. For example, differences can be determined between the cDNA or genomic sequence encoding elongase HSELO1-like protein in individuals afflicted with a disease and in normal individuals. If a mutation is observed in some or all of the afflicted individuals but not in normal individuals, then the mutation is likely to be the causative agent of the disease.

Sequence differences between a reference gene and a gene having mutations can be revealed by the direct DNA sequencing method. In addition, cloned DNA segments can be employed as probes to detect specific DNA segments. The sensitivity of this method is greatly enhanced when combined with PCR. For example, a sequencing primer can be used with a double-stranded PCR product or a single-stranded template molecule generated by a modified PCR. The sequence determination is performed by conventional procedures using radiolabeled nucleotides or by automatic sequencing procedures using fluorescent tags.

Genetic testing based on DNA sequence differences can be carried out by detection of alteration in electrophoretic mobility of DNA fragments in gels with or without denaturing agents. Small sequence deletions and insertions can be visualized, for example, by high resolution gel electrophoresis. DNA fragments of different sequences can be distinguished on denaturing formamide gradient gels in which the mobilities of different DNA fragments are retarded in the gel at different positions according to their specific melting or partial melting temperatures (*see, e.g.*, Myers *et al.*, *Science 230*, 1242, 1985). Sequence changes at specific locations can also be revealed by nuclease protection assays, such as RNase and S 1 protection or the chemical cleavage method (*e.g.*, Cotton *et al.*, *Proc. Natl. Acad. Sci. USA 85*, 4397-4401, 1985). Thus, the detection of a specific DNA sequence can be performed

by methods such as hybridization, RNase protection, chemical cleavage, direct DNA sequencing or the use of restriction enzymes and Southern blotting of genomic DNA. In addition to direct methods such as gel-electrophoresis and DNA sequencing, mutations can also be detected by *in situ* analysis.

Altered levels of elongase HSELO1-like protein also can be detected in various tissues. Assays used to detect levels of the receptor polypeptides in a body sample, such as blood or a tissue biopsy, derived from a host are well known to those of skill in the art and include radioimmunoassays, competitive binding assays, Western blot analysis, and ELISA assays.

All patents and patent applications cited in this disclosure are expressly incorporated herein by reference. The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples, which are provided for purposes of illustration only and are not intended to limit the scope of the invention.

EXAMPLE 1

Detection of elongase HSELO1-like protein activity

The polynucleotide of SEQ ID NO: 1 is inserted into the expression vector pCEV4 and the expression vector pCEV4-elongase HSELO1-like protein polypeptide obtained is transfected into human embryonic kidney 293 cells. From these cells extracts are obtained and elongase activity iss measured in a volume of 200µl containing 50 mM Tris (pH 7.5), 1mM MgC12, 150µM Triton X-100, 1 mM NADPH, 1 mM NADH, 10 mM betamercaptoethanol, 40 µM acyl-CoA acceptor (either palmitoyl-CoA, stearoyl-CoA, or eicosanoyl-CoA), and 60 µM [2-14] malonyl-CoA (0.05 µCi/ml) at 37°C. The reaction is initiated by the addition of 0.3 to 1.0 mg of the cell extract. Protein concentrations are determined using the Bio-rad protein assay reagent (Bio-Laboratories, Hercules, Calif.). At various times, the reaction iss terminated by adding 200µl of 5 M KOH-10% methanol MeOH and heating at 80°C for 1 h. Following addition of 200 µl of 10 N H2SO4, fatty acids are recovered by two 1.5-ml extractions into hexane. The extracted fatty acids are resolved by silica gel TLC using hexane-diethyl ether-acetic (30:70:1) as the developing solvent. The radiolabeled fatty acids are detected and quantified using a PhosphorImager SI (Molecular Dynamics, Inc. , Sunnyvale, Calif.). It is shown that the polypeptide of SEQ ID NO: 2 has a elongase HSELO1-like protein activity.

EXAMPLE 2

Detection of elongase HSELO1-like protein activity

The polynucleotide of SEQ ID NO: 1 is inserted into the expression vector pCEV4 and the expression vector pCEV4-elongase HSELO1-like protein polypeptide obtained is transfected into human embryonic kidney 293 cells. From these cells extracts are obtained and it is shown that the polypeptide of SEQ ID NO: 2 has a elongase HSELO1-like protein activity.

EXAMPLE 3

Expression of recombinant human elongase HSELO1-like protein

The *Pichia pastoris* expression vector pPICZB (Invitrogen, San Diego, CA) is used to produce large quantities of recombinant human elongase HSELO1-like polypeptides in yeast. The elongase HSELO1-like protein-encoding DNA sequence is derived from SEQ ID NO:1. Before insertion into vector pPICZB, the DNA sequence is modified by well known methods in such a way that it contains at its 5'-end an initiation codon and at its 3'-end an enterokinase cleavage site, a His6 reporter tag and a termination codon. Moreover, at both termini recognition sequences for restriction endonucleases are added and after digestion of the multiple cloning site of pPICZ B with the corresponding restriction enzymes the modified DNA sequence is ligated into pPICZB. This expression vector is designed for inducible expression in *Pichia pastoris*, driven by a yeast promoter. The resulting pPICZ/md-His6 vector is used to transform the yeast.

The yeast is cultivated under usual conditions in 5 liter shake flasks and the recombinantly produced protein isolated from the culture by affinity chromatography (Ni-NTA-Resin) in the presence of 8 M urea. The bound polypeptide is eluted with buffer, pH 3.5, and neutralized. Separation of the polypeptide from the His6 reporter tag is accomplished by site-specific proteolysis using enterokinase (Invitrogen, San Diego, CA) according to manufacturer's instructions. Purified human elongase HSELO1-like polypeptide is obtained.

EXAMPLE 4

Identification of test compounds that bind to elongase HSELO1-like polypeptides

Purified elongase HSELO1-like polypeptides comprising a glutathione-S-transferase protein and absorbed onto glutathione-derivatized wells of 96-well microtiter plates are contacted with test compounds from a small molecule library at pH 7.0 in a physiological buffer solution. Human elongase HSELO1-like polypeptides comprise

the amino acid sequence shown in SEQ ID NO:2. The test compounds comprise a fluorescent tag. The samples are incubated for 5 minutes to one hour. Control samples are incubated in the absence of a test compound.

The buffer solution containing the test compounds is washed from the wells. Binding of a test compound to an elongase HSELO1-like polypeptide is detected by fluorescence measurements of the contents of the wells. A test compound that increases the fluorescence in a well by at least 15% relative to fluorescence of a well in which a test compound is not incubated is identified as a compound which binds to an elongase HSELO1-like polypeptide.

EXAMPLE 5

Identification of a test compound which decreases elongase HSELO1-like gene expression

A test compound is administered to a culture of human cells transfected with an elongase HSELO1-like protein expression construct and incubated at 37 °C for 10 to 45 minutes. A culture of the same type of cells that have not been transfected is incubated for the same time without the test compound to provide a negative control.

RNA is isolated from the two cultures as described in Chirgwin *et al.*, *Biochem. 18*, 5294-99, 1979). Northern blots are prepared using 20 to 30 µg total RNA and hybridized with a ^{32}P-labeled elongase HSELO1-like protein-specific probe at 65 ° C in Express-hyb (CLONTECH). The probe comprises at least 11 contiguous nucleotides selected from the complement of SEQ ID NO:1. A test compound that decreases the elongase HSELO1-like protein-specific signal relative to the signal obtained in the absence of the test compound is identified as an inhibitor of elongase HSELO1-like gene expression.

EXAMPLE 6

Identification of a test compound which decreases elongase HSELO1-like protein activity

A test compound is administered to a culture of human cells transfected with an elongase HSELO1-like protein expression construct and incubated at 37 °C for 10 to 45 minutes. A culture of the same type of cells that have not been transfected is incubated for the same time without the test compound to provide a negative control. Elongase HSELO1-like protein activity is measured using a method of Ghioni *et al.*, Biochim Biophys Acta 1999 Feb 25;1437(2):170-81; Tocher, Lipids 1993 Apr;28(4):267-72; or Chang *et al.*, J Nutr 1992 Nov;122(11):2074-80.

A test compound which decreases the elongase HSELO1-like protein activity of the elongase HSELO1-like protein relative to the elongase HSELO1-like protein activity in the absence of the test compound is identified as an inhibitor of elongase HSELO1-like protein activity.

EXAMPLE 7

Tissue-specific expression of elongase HSELO1-like protein

The qualitative expression pattern of elongase HSELO1-like protein in various tissues is determined by Reverse Transcription-Polymerase Chain Reaction (RT-PCR).

To demonstrate that elongase HSELO1-like protein is involved in CNS disorders, the following tissues are screened: fetal and adult brain, muscle, heart, lung, kidney, liver, thymus, testis, colon, placenta, trachea, pancreas, kidney, gastric mucosa, colon, liver, cerebellum, skin, cortex (Alzheimer's and normal), hypothalamus, cortex, amygdala, cerebellum, hippocampus, choroid, plexus, thalamus, and spinal cord.

To demonstrate that elongase HSELO1-like protein is involved in cancer, expression is determined in the following tissues: adrenal gland, bone marrow, brain, cerebellum, colon, fetal brain, fetal liver, heart, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thymus, thyroid, trachea, uterus, and peripheral blood lymphocytes. Expression in the following cancer cell lines also is determined: DU-145 (prostate), NCI-H125 (lung), HT-29 (colon), COLO-205 (colon), A-549 (lung), NCI-H460 (lung), HT-116 (colon), DLD-1 (colon), MDA-MD-231 (breast), LS174T (colon), ZF-75 (breast), MDA-MN-435 (breast), HT-1080, MCF-7 (breast), and U87. Matched pairs of malignant and normal tissue from the same patient also are tested.

To demonstrate that elongase HSELO1-like protein is involved in the disease process of diabetes, the following whole body panel is screened to show predominant or relatively high expression: subcutaneous and mesenteric adipose tissue, adrenal gland, bone marrow, brain, colon, fetal brain, heart, hypothalamus, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal muscle, small intestine, spleen, stomach, testis, thymus, thyroid, trachea, and uterus. Human islet cells and an islet cell library also are tested. As a final step, the expression of elongase HSELO1-like protein in cells derived from normal individuals with the expression of cells derived from diabetic individuals is compared.

Quantitative expression profiling. Quantitative expression profiling is performed by the form of quantitative PCR analysis called "kinetic analysis" firstly described in Higuchi *et al.*, *BioTechnology 10*, 413-17, 1992, and Higuchi *et al.*, *BioTechnology 11*, 1026-30, 1993. The principle is that at any given cycle within the exponential phase of PCR, the amount of product is proportional to the initial number of template copies.

If the amplification is performed in the presence of an internally quenched fluorescent oligonucleotide (TaqMan probe) complementary to the target sequence, the probe is cleaved by the 5'-3' endonuclease activity of Taq DNA polymerase and a

fluorescent dye released in the medium (Holland *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 88*, 7276-80, 1991). Because the fluorescence emission will increase in direct proportion to the amount of the specific amplified product, the exponential growth phase of PCR product can be detected and used to determine the initial template concentration (Heid *et al.*, *Genome Res. 6*, 986-94, 1996, and Gibson *et al.*, *Genome Res. 6*, 995-1001, 1996).

The amplification of an endogenous control can be performed to standardize the amount of sample RNA added to a reaction. In this kind of experiment, the control of choice is the 18S ribosomal RNA. Because reporter dyes with differing emission spectra are available, the target and the endogenous control can be independently quantified in the same tube if probes labeled with different dyes are used.

All "real time PCR" measurements of fluorescence are made in the ABI Prism 7700.

RNA extraction and cDNA preparation. Total RNA from the tissues listed above are used for expression quantification. RNAs labeled "from autopsy" were extracted from autoptic tissues with the TRIzol reagent (Life Technologies, MD) according to the manufacturer's protocol.

Fifty µg of each RNA were treated with DNase I for 1 hour at 37 C in the following reaction mix: 0.2 U/µl RNase-free DNase I (Roche Diagnostics, Germany); 0.4 U/µl RNase inhibitor (PE Applied Biosystems, CA); 10 mM Tris-HCl pH 7.9; 10mM $MgCl_2$; 50 mM NaCl; and 1 mM DTT.

After incubation, RNA is extracted once with 1 volume of phenol:chloroform:isoamyl alcohol (24:24:1) and once with chloroform, and precipitated with 1/10 volume of 3 M NaAcetate, pH5.2, and 2 volumes of ethanol.

Fifty µg of each RNA from the autoptic tissues are DNase treated with the DNA-free kit purchased from Ambion (Ambion, TX). After resuspension and spectro-

photometric quantification, each sample is reverse transcribed with the TaqMan Reverse Transcription Reagents (PE Applied Biosystems, CA) according to the manufacturer's protocol. The final concentration of RNA in the reaction mix is 200ng/µL. Reverse transcription is carried out with 2.5µM of random hexamer primers.

TaqMan quantitative analysis. Specific primers and probe are designed according to the recommendations of PE Applied Biosystems; the probe can be labeled at the 5' end FAM (6-carboxy-fluorescein) and at the 3' end with TAMRA (6-carboxy-tetramethyl-rhodamine). Quantification experiments are performed on 10 ng of reverse transcribed RNA from each sample. Each determination is done in triplicate.

Total cDNA content is normalized with the simultaneous quantification (multiplex PCR) of the 18S ribosomal RNA using the Pre-Developed TaqMan Assay Reagents (PDAR) Control Kit (PE Applied Biosystems, CA).

The assay reaction mix is as follows: 1X final TaqMan Universal PCR Master Mix (from 2X stock) (PE Applied Biosystems, CA); 1X PDAR control – 18S RNA (from 20X stock); 300 nM forward primer; 900 nM reverse primer; 200 nM probe; 10 ng cDNA; and water to 25 µl.

Each of the following steps are carried out once: pre PCR, 2 minutes at 50°C, and 10 minutes at 95°C. The following steps are carried out 40 times: denaturation, 15 seconds at 95°C, annealing/extension, 1 minute at 60°C.

The experiment is performed on an ABI Prism 7700 Sequence Detector (PE Applied Biosystems, CA). At the end of the run, fluorescence data acquired during PCR are processed as described in the ABI Prism 7700 user's manual in order to achieve better background subtraction as well as signal linearity with the starting target quantity.

EXAMPLE 8

Diabetes: In vivo testing of compounds/target validation

1. Glucose Production:

Over-production of glucose by the liver, due to an enhanced rate of gluconeogenesis, is the major cause of fasting hyperglycemia in diabetes. Overnight fasted normal rats or mice have elevated rates of gluconeogenesis as do streptozotocin-induced diabetic rats or mice fed ad libitum. Rats are made diabetic with a single intravenous injection of 40 mg/kg of streptozotocin while C57BL/KsJ mice are given 40-60 mg/kg i.p. for 5 consecutive days. Blood glucose is measured from tail-tip blood and then compounds are administered via different routes (p.o., i.p., i.v., s.c.). Blood is collected at various times thereafter and glucose measured. Alternatively, compounds are administered for several days, then the animals are fasted overnight, blood is collected and plasma glucose measured. Compounds that inhibit glucose production will decrease plasma glucose levels compared to the vehicle-treated control group.

2. Insulin Sensitivity:

Both ob/ob and db/db mice as well as diabetic Zucker rats are hyperglycemic, hyperinsulinemic and insulin resistant. The animals are pre-bled, their glucose levels measured, and then they are grouped so that the mean glucose level is the same for each group. Compounds are administered daily either q.d. or b.i.d. by different routes (p.o., i.p., s.c.) for 7-28 days. Blood is collected at various times and plasma glucose and insulin levels determined. Compounds that improve insulin sensitivity in these models will decrease both plasma glucose and insulin levels when compared to the vehicle-treated control group.

3. Insulin Secretion:

Compounds that enhance insulin secretion from the pancreas will increase plasma insulin levels and improve the disappearance of plasma glucose following the administration of a glucose load. When measuring insulin levels, compounds are administered by different routes (p.o., i.p., s.c. or i.v.) to overnight fasted normal rats or mice. At the appropriate time an intravenous glucose load (0.4g/kg) is given, blood is collected one minute later. Plasma insulin levels are determined. Compounds that enhance insulin secretion will increase plasma insulin levels compared to animals given only glucose. When measuring glucose disappearance, animals are bled at the appropriate time after compound administration, then given either an oral or intraperitoneal glucose load (1g/kg), bled again after 15, 30, 60 and 90 minutes and plasma glucose levels determined. Compounds that increase insulin levels will decrease glucose levels and the area-under-the glucose curve when compared to the vehicle-treated group given only glucose.

Compounds that enhance insulin secretion from the pancreas will increase plasma insulin levels and improve the disappearance of plasma glucose following the administration of a glucose load. When measuring insulin levels, test compounds which regulate elongase HSELO1-like protein are administered by different routes (p.o., i.p., s.c., or i.v.) to overnight fasted normal rats or mice. At the appropriate time an intravenous glucose load (0.4g/kg) is given, blood is collected one minute later. Plasma insulin levels are determined. Test compounds that enhance insulin secretion will increase plasma insulin levels compared to animals given only glucose. When measuring glucose disappearance, animals are bled at the appropriate time after compound administration, then given either an oral or intraperitoneal glucose load (1g/kg), bled again after 15, 30, 60, and 90 minutes and plasma glucose levels determined. Test compounds that increase insulin levels will decrease glucose levels and the area-under-the glucose curve when compared to the vehicle-treated group given only glucose.

4. Glucose Production:

Over-production of glucose by the liver, due to an enhanced rate of gluconeogenesis, is the major cause of fasting hyperglycemia in diabetes. Overnight fasted normal rats or mice have elevated rates of gluconeogenesis as do streptozotocin-induced diabetic rats or mice fed ad libitum. Rats are made diabetic with a single intravenous injection of 40 mg/kg of streptozotocin while C57BL/KsJ mice are given 40-60 mg/kg i.p. for 5 consecutive days. Blood glucose is measured from tail-tip blood and then compounds are administered via different routes (p.o., i.p., i.v., s.c.). Blood is collected at various times thereafter and glucose measured. Alternatively, compounds are administered for several days, then the animals are fasted overnight, blood is collected and plasma glucose measured. Compounds that inhibit glucose production will decrease plasma glucose levels compared to the vehicle-treated control group.

5. Insulin Sensitivity:

Both ob/ob and db/db mice as well as diabetic Zucker rats are hyperglycemic, hyperinsulinemic and insulin resistant. The animals are pre-bled, their glucose levels measured, and then they are grouped so that the mean glucose level is the same for each group. Compounds are administered daily either q.d. or b.i.d. by different routes (p.o., i.p., s.c.) for 7-28 days. Blood is collected at various times and plasma glucose and insulin levels determined. Compounds that improve insulin sensitivity in these models will decrease both plasma glucose and insulin levels when compared to the vehicle-treated control group.

6. Insulin Secretion:

Compounds that enhance insulin secretion from the pancreas will increase plasma insulin levels and improve the disappearance of plasma glucose following the administration of a glucose load. When measuring insulin levels, compounds are

administered by different routes (p.o., i.p., s.c. or i.v.) to overnight fasted normal rats or mice. At the appropriate time an intravenous glucose load (0.4g/kg) is given, blood is collected one minute later. Plasma insulin levels are determined. Compounds that enhance insulin secretion will increase plasma insulin levels compared to animals given only glucose. When measuring glucose disappearance, animals are bled at the appropriate time after compound administration, then given either an oral or intraperitoneal glucose load (1g/kg), bled again after 15, 30, 60 and 90 minutes and plasma glucose levels determined. Compounds that increase insulin levels will decrease glucose levels and the area-under-the glucose curve when compared to the vehicle-treated group given only glucose.

EXAMPLE 9

In vivo testing of compounds/target validation

1. Pain:

Acute Pain

Acute pain is measured on a hot plate mainly in rats. Two variants of hot plate testing are used: In the classical variant animals are put on a hot surface (52 to 56 °C) and the latency time is measured until the animals show nocifensive behavior, such as stepping or foot licking. The other variant is an increasing temperature hot plate where the experimental animals are put on a surface of neutral temperature. Subsequently this surface is slowly but constantly heated until the animals begin to lick a hind paw. The temperature which is reached when hind paw licking begins is a measure for pain threshold.

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Persistent Pain

Persistent pain is measured with the formalin or capsaicin test, mainly in rats. A solution of 1 to 5% formalin or 10 to 100 µg capsaicin is injected into one hind paw of the experimental animal. After formalin or capsaicin application the animals show nocifensive reactions like flinching, licking and biting of the affected paw. The number of nocifensive reactions within a time frame of up to 90 minutes is a measure for intensity of pain.

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to formalin or capsaicin administration.

Neuropathic Pain

Neuropathic pain is induced by different variants of unilateral sciatic nerve injury mainly in rats. The operation is performed under anesthesia. The first variant of sciatic nerve injury is produced by placing loosely constrictive ligatures around the common sciatic nerve. The second variant is the tight ligation of about the half of the diameter of the common sciatic nerve. In the next variant, a group of models is used in which tight ligations or transections are made of either the L5 and L6 spinal nerves, or the L% spinal nerve only. The fourth variant involves an axotomy of two of the three terminal branches of the sciatic nerve (tibial and common peroneal nerves) leaving the remaining sural nerve intact whereas the last variant comprises the axotomy of only the tibial branch leaving the sural and common nerves uninjured. Control animals are treated with a sham operation.

Postoperatively, the nerve injured animals develop a chronic mechanical allodynia, cold allodynioa, as well as a thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA; Electronic von Frey

System, Somedic Sales AB, Hörby, Sweden). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy), or by means of a cold plate of 5 to 10 °C where the nocifensive reactions of the affected hind paw are counted as a measure of pain intensity. A further test for cold induced pain is the counting of nocifensive reactions, or duration of nocifensive responses after plantar administration of acetone to the affected hind limb. Chronic pain in general is assessed by registering the circadanian rhythms in activity (Surjo and Arndt, Universität zu Köln, Cologne, Germany), and by scoring differences in gait (foot print patterns; FOOTPRINTS program, Klapdor et al., 1997. A low cost method to analyze footprint patterns. J. Neurosci. Methods 75, 49-54).

Compounds are tested against sham operated and vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Inflammatory Pain

Inflammatory pain is induced mainly in rats by injection of 0.75 mg carrageenan or complete Freund's adjuvant into one hind paw. The animals develop an edema with mechanical allodynia as well as thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy, Paw thermal stimulator, G. Ozaki, University of California, USA). For edema measurement two methods are being used. In the first method, the animals are sacrificed and the affected hindpaws sectioned and weighed. The second method comprises differences in paw volume by measuring water displacement in a plethysmometer (Ugo Basile, Comerio, Italy).

Compounds are tested against uninflamed as well as vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Diabetic Neuropathic Pain

Rats treated with a single intraperitoneal injection of 50 to 80 mg/kg streptozotocin develop a profound hyperglycemia and mechanical allodynia within 1 to 3 weeks. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, ITC Inc.-Life Science Instruments, Woodland Hills, SA, USA).

Compounds are tested against diabetic and non-diabetic vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

2. Parkinson's disease

6-Hydroxydopamine (6-OH-DA) Lesion

Degeneration of the dopaminergic nigrostriatal and striatopallidal pathways is the central pathological event in Parkinson's disease. This disorder has been mimicked experimentally in rats using single/sequential unilateral stereotaxic injections of 6-OH-DA into the medium forebrain bundle (MFB).

Male Wistar rats (Harlan Winkelmann, Germany), weighing 200±250 g at the beginning of the experiment, are used. The rats are maintained in a temperature- and humidity-controlled environment under a 12 h light/dark cycle with free access to food and water when not in experimental sessions. The following in vivo protocols are approved by the governmental authorities. All efforts are made to minimize

animal suffering, to reduce the number of animals used, and to utilize alternatives to in vivo techniques.

Animals are administered pargyline on the day of surgery (Sigma, St. Louis, MO, USA; 50 mg/kg i.p.) in order to inhibit metabolism of 6-OHDA by monoamine oxidase and desmethylimipramine HCl (Sigma; 25 mg/kg i.p.) in order to prevent uptake of 6-OHDA by noradrenergic terminals. Thirty minutes later the rats are anesthetized with sodium pentobarbital (50 mg/kg) and placed in a stereotaxic frame. In order to lesion the DA nigrostriatal pathway 4 µl of 0.01% ascorbic acid-saline containing 8 µg of 6-OHDA HBr (Sigma) are injected into the left medial fore-brain bundle at a rate of 1 µl/min (2.4 mm anterior, 1.49 mm lateral, -2.7 mm ventral to Bregma and the skull surface). The needle is left in place an additional 5 min to allow diffusion to occur.

Stepping Test

Forelimb akinesia is assessed three weeks following lesion placement using a modified stepping test protocol. In brief, the animals are held by the experimenter with one hand fixing the hindlimbs and slightly raising the hind part above the surface. One paw is touching the table, and is then moved slowly sideways (5 s for 1 m), first in the forehand and then in the backhand direction. The number of adjusting steps is counted for both paws in the backhand and forehand direction of movement. The sequence of testing is right paw forehand and backhand adjusting stepping, followed by left paw forehand and backhand directions. The test is repeated three times on three consecutive days, after an initial training period of three days prior to the first testing. Forehand adjusted stepping reveals no consistent differences between lesioned and healthy control animals. Analysis is therefore restricted to backhand adjusted stepping.

Balance Test

Balance adjustments following postural challenge are also measured during the stepping test sessions. The rats are held in the same position as described in the stepping test and, instead of being moved sideways, tilted by the experimenter towards the side of the paw touching the table. This maneuver results in loss of balance and the ability of the rats to regain balance by forelimb movements is scored on a scale ranging from 0 to 3. Score 0 is given for a normal forelimb placement. When the forelimb movement is delayed but recovery of postural balance detected, score 1 is given. Score 2 represents a clear, yet insufficient, forelimb reaction, as evidenced by muscle contraction, but lack of success in recovering balance, and score 3 is given for no reaction of movement. The test is repeated three times a day on each side for three consecutive days after an initial training period of three days prior to the first testing.

Staircase Test (Paw Reaching)

A modified version of the staircase test is used for evaluation of paw reaching behavior three weeks following primary and secondary lesion placement. Plexiglass test boxes with a central platform and a removable staircase on each side are used. The apparatus is designed such that only the paw on the same side at each staircase can be used, thus providing a measure of independent forelimb use. For each test the animals are left in the test boxes for 15 min. The double staircase is filled with 7 x 3 chow pellets (Precision food pellets, formula: P, purified rodent diet, size 45 mg; Sandown Scientific) on each side. After each test the number of pellets eaten (successfully retrieved pellets) and the number of pellets taken (touched but dropped) for each paw and the success rate (pellets eaten/pellets taken) are counted separately. After three days of food deprivation (12 g per animal per day) the animals are tested for 11 days. Full analysis is conducted only for the last five days.

MPTP treatment

The neurotoxin 1-methyl-4-phenyl-1,2,3,6-tetrahydro-pyridine (MPTP) causes degeneration of mesencephalic dopaminergic (DAergic) neurons in rodents, non-human primates, and humans and, in so doing, reproduces many of the symptoms of Parkinson's disease. MPTP leads to a marked decrease in the levels of dopamine and its metabolites, and in the number of dopaminergic terminals in the striatum as well as severe loss of the tyrosine hydroxylase (TH)-immunoreactive cell bodies in the substantia nigra, pars compacta.

In order to obtain severe and long-lasting lesions, and to reduce mortality, animals receive single injections of MPTP, and are then tested for severity of lesion 7–10 days later. Successive MPTP injections are administered on days 1, 2 and 3. Animals receive application of 4 mg/kg MPTP hydrochloride (Sigma) in saline once daily. All injections are intraperitoneal (i.p.) and the MPTP stock solution is frozen between injections. Animals are decapitated on day 11.

Immunohistology

At the completion of behavioral experiments, all animals are anaesthetized with 3 ml thiopental (1 g/40 ml i.p., Tyrol Pharma). The mice are perfused transcardially with 0.01 M PBS (pH 7.4) for 2 min, followed by 4% paraformaldehyde (Merck) in PBS for 15 min. The brains are removed and placed in 4% paraformaldehyde for 24 h at 4 °C. For dehydration they are then transferred to a 20% sucrose (Merck) solution in 0.1 M PBS at 4 °C until they sink. The brains are frozen in methylbutan at -20 °C for 2 min and stored at -70 °C. Using a sledge microtome (mod. 3800-Frigocut, Leica), 25 µm sections are taken from the genu of the corpus callosum (AP 1.7 mm) to the hippocampus (AP 21.8 mm) and from AP 24.16 to AP 26.72. Forty-six sections are cut and stored in assorters in 0.25 M Tris buffer (pH 7.4) for immunohistochemistry.

A series of sections is processed for free-floating tyrosine hydroxylase (TH) immunohistochemistry. Following three rinses in 0.1 M PBS, endogenous peroxidase activity is quenched for 10 min in 0.3% H_2O_2 ±PBS. After rinsing in PBS, sections are preincubated in 10% normal bovine serum (Sigma) for 5 min as blocking agent and transferred to either primary anti-rat TH rabbit antiserum (dilution 1:2000).

Following overnight incubation at room temperature, sections for TH immunoreactivity are rinsed in PBS (2 x10 min) and incubated in biotinylated anti-rabbit immunoglobulin G raised in goat (dilution 1:200) (Vector) for 90 min, rinsed repeatedly and transferred to Vectastain ABC (Vector) solution for 1 h. 3,.3' -Diaminobenzidine tetrahydrochloride (DAB; Sigma) in 0.1 M PBS, supplemented with 0.005% H_2O_2 , serves as chromogen in the subsequent visualization reaction. Sections are mounted on to gelatin-coated slides, left to dry overnight, counter-stained with hematoxylin dehydrated in ascending alcohol concentrations and cleared in butylacetate. Coverslips are mounted on entellan.

Rotarod Test

We use a modification of the procedure described by Rozas and Labandeira-Garcia (1997), with a CR-1 Rotamex system (Columbus Instruments, Columbus, OH) comprising an IBM-compatible personal computer, a CIO-24 data acquisition card, a control unit, and a four-lane rotarod unit. The rotarod unit consists of a rotating spindle (diameter 7.3 cm) and individual compartments for each mouse. The system software allows preprogramming of session protocols with varying rotational speeds (0–80 rpm). Infrared beams are used to detect when a mouse has fallen onto the base grid beneath the rotarod. The system logs the fall as the end of the experiment for that mouse, and the total time on the rotarod, as well as the time of the fall and all the set-up parameters, are recorded. The system also allows a weak current to be passed through the base grid, to aid training.

3. Dementia

The object recognition task

The object recognition task has been designed to assess the effects of experimental manipulations on the cognitive performance of rodents. A rat is placed in an open field, in which two identical objects are present. The rats inspects both objects during the first trial of the object recognition task. In a second trial, after a retention interval of for example 24 hours, one of the two objects used in the first trial, the 'familiar' object, and a novel object are placed in the open field. The inspection time at each of the objects is registered. The basic measures in the OR task is the time spent by a rat exploring the two object the second trial. Good retention is reflected by higher exploration times towards the novel than the 'familiar' object.

Administration of the putative cognition enhancer prior to the first trial predominantly allows assessment of the effects on acquisition, and eventually on consolidation processes. Administration of the testing compound after the first trial allows to assess the effects on consolidation processes, whereas administration before the second trial allows to measure effects on retrieval processes.

The passive avoidance task

The passive avoidance task assesses memory performance in rats and mice. The inhibitory avoidance apparatus consists of a two-compartment box with a light compartment and a dark compartment. The two compartments are separated by a guillotine door that can be operated by the experimenter. A threshold of 2 cm separates the two compartments when the guillotine door is raised. When the door is open, the illumination in the dark compartment is about 2 lux. The light intensity is about 500 lux at the center of the floor of the light compartment.

Two habituation sessions, one shock session, and a retention session are given, separated by inter-session intervals of 24 hours. In the habituation sessions and the

retention session the rat is allowed to explore the apparatus for 300 sec. The rat is placed in the light compartment, facing the wall opposite to the guillotine door. After an accommodation period of 15 sec. the guillotine door is opened so that all parts of the apparatus can be visited freely. Rats normally avoid brightly lit areas and will enter the dark compartment within a few seconds.

In the shock session the guillotine door between the compartments is lowered as soon as the rat has entered the dark compartment with its four paws, and a scrambled 1 mA footshock is administered for 2 sec. The rat is removed from the apparatus and put back into its home cage. The procedure during the retention session is identical to that of the habituation sessions.

The step-through latency, that is the first latency of entering the dark compartment (in sec.) during the retention session is an index of the memory performance of the animal; the longer the latency to enter the dark compartment, the better the retention is. A testing compound in given half an hour before the shock session, together with 1 $mg*kg^{-1}$ scopolamine. Scopolamine impairs the memory performance during the retention session 24 hours later. If the test compound increases the enter latency compared with the scopolamine-treated controls, is likely to possess cognition enhancing potential.

The Morris water escape task

The Morris water escape task measures spatial orientation learning in rodents. It is a test system that has extensively been used to investigate the effects of putative therapeutic on the cognitive functions of rats and mice. The performance of an animal is assessed in a circular water tank with an escape platform that is submerged about 1 cm below the surface of the water. The escape platform is not visible for an animal swimming in the water tank. Abundant extra-maze cues are provided by the furniture in the room, including desks, computer equipment, a second water tank, the presence of the experimenter, and by a radio on a shelf that is playing softly.

The animals receive four trials during five daily acquisition sessions. A trial is started by placing an animal into the pool, facing the wall of the tank. Each of four starting positions in the quadrants north, east, south, and west is used once in a series of four trials; their order is randomized. The escape platform is always in the same position. A trial is terminated as soon as the animal had climbs onto the escape platform or when 90 seconds have elapsed, whichever event occurs first. The animal is allowed to stay on the platform for 30 seconds. Then it is taken from the platform and the next trial is started. If an animal did not find the platform within 90 seconds it is put on the platform by the experimenter and is allowed to stay there for 30 seconds. After the fourth trial of the fifth daily session, an additional trial is given as a probe trial: the platform is removed, and the time the animal spends in the four quadrants is measured for 30 or 60 seconds. In the probe trial, all animals start from the same start position, opposite to the quadrant where the escape platform had been positioned during acquisition.

Four different measures are taken to evaluate the performance of an animal during acquisition training: escape latency, traveled distance, distance to platform, and swimming speed. The following measures are evaluated for the probe trial: time (s) in quadrants and traveled distance (cm) in the four quadrants. The probe trial provides additional information about how well an animal learned the position of the escape platform. If an animal spends more time and swims a longer distance in the quadrant where the platform had been positioned during the acquisition sessions than in any other quadrant, one concludes that the platform position has been learned well.

In order to assess the effects of putative cognition enhancing compounds, rats or mice with specific brain lesions which impair cognitive functions, or animals treated with compounds such as scopolamine or MK-801, which interfere with normal learning, or aged animals which suffer from cognitive deficits, are used.

The T-maze spontaneous alternation task

The T-maze spontaneous alternation task (TeMCAT) assesses the spatial memory performance in mice. The start arm and the two goal arms of the T-maze are provided with guillotine doors which can be operated manually by the experimenter. A mouse is put into the start arm at the beginning of training. The guillotine door is closed. In the first trial, the 'forced trial', either the left or right goal arm is blocked by lowering the guillotine door. After the mouse has been released from the start arm, it will negotiate the maze, eventually enter the open goal arm, and return to the start position, where it will be confined for 5 seconds, by lowering the guillotine door. Then, the animal can choose freely between the left and right goal arm (all guillotine-doors opened) during 14 'free choice' trials. As soon a the mouse has entered one goal arm, the other one is closed. The mouse eventually returns to the start arm and is free to visit whichever go alarm it wants after having been confined to the start arm for 5 seconds. After completion of 14 free choice trials in one session, the animal is removed from the maze. During training, the animal is never handled.

The percent alternations out of 14 trials is calculated. This percentage and the total time needed to complete the first forced trial and the subsequent 14 free choice trials (in s) is analyzed. Cognitive deficits are usually induced by an injection of scopolamine, 30 min before the start of the training session. Scopolamine reduced the per-cent alternations to chance level, or below. A cognition enhancer, which is always administered before the training session, will at least partially, antagonize the scopolamine-induced reduction in the spontaneous alternation rate.

EXAMPLE 10

Proliferation inhibition assay: Antisense oligonucleotides suppress the growth of cancer cell lines

The cell line used for testing is the human colon cancer cell line HCT116. Cells are cultured in RPMI-1640 with 10-15% fetal calf serum at a concentration of 10,000 cells per milliliter in a volume of 0.5 ml and kept at 37 °C in a 95% air/5%CO_2 atmosphere.

Phosphorothioate oligoribonucleotides are synthesized on an Applied Biosystems Model 380B DNA synthesizer using phosphoroamidite chemistry. A sequence of 24 bases complementary to the nucleotides at position 1 to 24 of SEQ ID NO:1 is used as the test oligonucleotide. As a control, another (random) sequence is used: 5'-TCA ACT GAC TAG ATG TAC ATG GAC-3' (SEQ ID NO:23). Following assembly and deprotection, oligonucleotides are ethanol-precipitated twice, dried, and suspended in phosphate buffered saline at the desired concentration. Purity of the oligonucleotides is tested by capillary gel electrophoresis and ion exchange HPLC. The purified oligonucleotides are added to the culture medium at a concentration of 10 μM once per day for seven days.

The addition of the test oligonucleotide for seven days results in significantly reduced expression of human elongase HSELO1-like protein as determined by Western blotting. This effect is not observed with the control oligonucleotide. After 3 to 7 days, the number of cells in the cultures is counted using an automatic cell counter. The number of cells in cultures treated with the test oligonucleotide (expressed as 100%) is compared with the number of cells in cultures treated with the control oligonucleotide. The number of cells in cultures treated with the test oligonucleotide is not more than 30% of control, indicating that the inhibition of human elongase HSELO1-like protein has an anti-proliferative effect on cancer cells.

EXAMPLE 11

In vivo testing of compounds/target validation

1. Acute Mechanistic Assays

1.1. Reduction in Mitogenic Plasma Hormone Levels

This non-tumor assay measures the ability of a compound to reduce either the endogenous level of a circulating hormone or the level of hormone produced in response to a biologic stimulus. Rodents are administered test compound (p.o., i.p., i.v., i.m., or s.c.). At a predetermined time after administration of test compound, blood plasma is collected. Plasma is assayed for levels of the hormone of interest. If the normal circulating levels of the hormone are too low and/or variable to provide consistent results, the level of the hormone may be elevated by a pre-treatment with a biologic stimulus (i.e., LHRH may be injected i.m. into mice at a dosage of 30 ng/mouse to induce a burst of testosterone synthesis). The timing of plasma collection would be adjusted to coincide with the peak of the induced hormone response. Compound effects are compared to a vehicle-treated control group. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test. Significance is p value ≤ 0.05 compared to the vehicle control group.

1.2. Hollow Fiber Mechanism of Action Assay

Hollow fibers are prepared with desired cell line(s) and implanted intraperitoneally and/or subcutaneously in rodents. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Fibers are harvested in accordance with specific readout assay protocol, these may include assays for gene expression (bDNA, PCR, or Taqman), or a specific biochemical activity (i.e., cAMP levels. Results are analyzed by Student's t-test or Rank Sum test after the variance between groups is compared by an F-test, with significance at $p \leq 0.05$ as compared to the vehicle control group.

2. Subacute Functional *In Vivo* Assays

2.1. Reduction in Mass of Hormone Dependent Tissues

This is another non-tumor assay that measures the ability of a compound to reduce the mass of a hormone dependent tissue (i.e., seminal vesicles in males and uteri in females). Rodents are administered test compound (p.o., i.p., i.v., i.m., or s.c.)

according to a predetermined schedule and for a predetermined duration (i.e., 1 week). At termination of the study, animals are weighed, the target organ is excised, any fluid is expressed, and the weight of the organ is recorded. Blood plasma may also be collected. Plasma may be assayed for levels of a hormone of interest or for levels of test agent. Organ weights may be directly compared or they may be normalized for the body weight of the animal. Compound effects are compared to a vehicle-treated control group. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test. Significance is p value ≤ 0.05 compared to the vehicle control group.

2.2. Hollow Fiber Proliferation Assay

Hollow fibers are prepared with desired cell line(s) and implanted intraperitoneally and/or subcutaneously in rodents. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Fibers are harvested in accordance with specific readout assay protocol. Cell proliferation is determined by measuring a marker of cell number (i.e., MTT or LDH). The cell number and change in cell number from the starting inoculum are analyzed by Student's t-test or Rank Sum test after the variance between groups is compared by an F-test, with significance at $p \leq 0.05$ as compared to the vehicle control group.

2.3. Anti-angiogenesis Models

2.3.1. Corneal Angiogenesis

Hydron pellets with or without growth factors or cells are implanted into a micropocket surgically created in the rodent cornea. Compound administration may be systemic or local (compound mixed with growth factors in the hydron pellet). Corneas are harvested at 7 days post implantation immediately following intracardiac infusion of colloidal carbon and are fixed in 10% formalin. Readout is qualitative scoring and/or image analysis. Qualitative scores are compared by Rank Sum test. Image analysis data is evaluated by measuring the area of neovascularization (in

pixels) and group averages are compared by Student's t-test (2 tail). Significance is $p \leq 0.05$ as compared to the growth factor or cells only group.

2.3.2. Matrigel Angiogenesis

Matrigel, containing cells or growth factors, is injected subcutaneously. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Matrigel plugs are harvested at predetermined time point(s) and prepared for readout. Readout is an ELISA-based assay for hemoglobin concentration and/or histological examination (i.e. vessel count, special staining for endothelial surface markers: CD31, factor-8). Readouts are analyzed by Student's t-test, after the variance between groups is compared by an F-test, with significance determined at $p \leq 0.05$ as compared to the vehicle control group.

3. Primary Antitumor Efficacy

3.1. Early Therapy Models

3.1.1. Subcutaneous Tumor

Tumor cells or fragments are implanted subcutaneously on Day 0. Vehicle and/or compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule starting at a time, usually on Day 1, prior to the ability to measure the tumor burden. Body weights and tumor measurements are recorded 2-3 times weekly. Mean net body and tumor weights are calculated for each data collection day. Anti-tumor efficacy may be initially determined by comparing the size of treated (T) and control (C) tumors on a given day by a Student's t-test, after the variance between groups is compared by an F-test, with significance determined at $p \leq 0.05$. The experiment may also be continued past the end of dosing in which case tumor measurements would continue to be recorded to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-

Meier curves from the times for individual tumors to attain the evaluation size. Significance is $p \leq 0.05$.

3.1.2. Intraperitoneal/Intracranial Tumor Models

Tumor cells are injected intraperitoneally or intracranially on Day 0. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule starting on Day 1. Observations of morbidity and/or mortality are recorded twice daily. Body weights are measured and recorded twice weekly. Morbidity/mortality data is expressed in terms of the median time of survival and the number of long-term survivors is indicated separately. Survival times are used to generate Kaplan-Meier curves. Significance is $p \leq 0.05$ by a log-rank test compared to the control group in the experiment.

3.2. Established Disease Model

Tumor cells or fragments are implanted subcutaneously and grown to the desired size for treatment to begin. Once at the predetermined size range, mice are randomized into treatment groups. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Tumor and body weights are measured and recorded 2-3 times weekly. Mean tumor weights of all groups over days post inoculation are graphed for comparison. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. Tumor measurements may be recorded after dosing has stopped to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is p value≤ 0.05 compared to the vehicle control group.

3.3. Orthotopic Disease Models

3.3.1. Mammary Fat Pad Assay

Tumor cells or fragments, of mammary adenocarcinoma origin, are implanted directly into a surgically exposed and reflected mammary fat pad in rodents. The fat pad is placed back in its original position and the surgical site is closed. Hormones may also be administered to the rodents to support the growth of the tumors. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Tumor and body weights are measured and recorded 2-3 times weekly. Mean tumor weights of all groups over days post inoculation are graphed for comparison. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group.

Tumor measurements may be recorded after dosing has stopped to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is p value≤ 0.05 compared to the vehicle control group. In addition, this model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ, or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

3.3.2. Intraprostatic Assay

Tumor cells or fragments, of prostatic adenocarcinoma origin, are implanted directly into a surgically exposed dorsal lobe of the prostate in rodents. The prostate is externalized through an abdominal incision so that the tumor can be implanted specifically in the dorsal lobe while verifying that the implant does not enter the seminal vesicles. The successfully inoculated prostate is replaced in the abdomen and the incisions through the abdomen and skin are closed. Hormones may also be administered to the rodents to support the growth of the tumors. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ (i.e., the lungs), or measuring the target organ weight (i.e., the regional lymph nodes). The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

3.3.3. Intrabronchial Assay

Tumor cells of pulmonary origin may be implanted intrabronchially by making an incision through the skin and exposing the trachea. The trachea is pierced with the beveled end of a 25 gauge needle and the tumor cells are inoculated into the main bronchus using a flat-ended 27 gauge needle with a 90° bend. Compounds are

administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ (i.e., the contralateral lung), or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

3.3.4. Intracecal Assay

Tumor cells of gastrointestinal origin may be implanted intracecally by making an abdominal incision through the skin and externalizing the intestine. Tumor cells are inoculated into the cecal wall without penetrating the lumen of the intestine using a 27 or 30 gauge needle. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ (i.e., the liver), or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test,

with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

4. Secondary (Metastatic) Antitumor Efficacy

4.1. Spontaneous Metastasis

Tumor cells are inoculated s.c. and the tumors allowed to grow to a predetermined range for spontaneous metastasis studies to the lung or liver. These primary tumors are then excised. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule which may include the period leading up to the excision of the primary tumor to evaluate therapies directed at inhibiting the early stages of tumor metastasis. Observations of morbidity and/or mortality are recorded daily. Body weights are measured and recorded twice weekly. Potential endpoints include survival time, numbers of visible foci per target organ, or target organ weight. When survival time is used as the endpoint the other values are not determined. Survival data is used to generate Kaplan-Meier curves. Significance is $p \leq 0.05$ by a log-rank test compared to the control group in the experiment. The mean number of visible tumor foci, as determined under a dissecting microscope, and the mean target organ weights are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment for both of these endpoints.

4.2. Forced Metastasis

Tumor cells are injected into the tail vein, portal vein, or the left ventricle of the heart in experimental (forced) lung, liver, and bone metastasis studies, respectively. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Observations of morbidity and/or mortality are recorded daily. Body weights are measured and recorded twice weekly. Potential endpoints include survival time, numbers of visible foci per target organ, or target organ weight. When survival time is used as the endpoint the other values are not determined. Survival

data is used to generate Kaplan-Meier curves. Significance is $p \leq 0.05$ by a log-rank test compared to the control group in the experiment. The mean number of visible tumor foci, as determined under a dissecting microscope, and the mean target organ weights are compared by Student's t-test after conducting an F-test, with significance at $p \leq 0.05$ compared to the vehicle control group in the experiment for both endpoints.

EXAMPLE 12

Total RNA used for Taqman quantitative analysis were either purchased (Clontech,CA) or extracted from tissues using TRIzol reagent (Life Technologies, MD) according to a modified vendor protocol which utilizes the Rneasy protocol (Qiagen, CA)

One hundred µg of each RNA were treated with DNase I using RNase free- DNase (Qiagen, CA) for use with RNeasy or QiaAmp columns.

After elution and quantitation with Ribogreen (Molecular Probes Inc., OR), each sample was reverse transcribed using the GibcoBRL Superscript II First Strand Synthesis System for RT-PCR according to vendor protocol (Life Technologies, MD). The final concentration of RNA in the reaction mix was 50ng/µL. Reverse transcription was performed with 50 ng of random hexamers.

Specific primers and probe were designed according to PE Applied Biosystems' Primer Express program recommendations and are listed below:

forward primer: 5'-(GCAGTTCGTGCTCACCATCA)-3'
reverse primer: 5'-(ACGTTAGCATATAAGATGACTGGAAGAT)-3'
probe: SYBR Green

Quantitation experiments were performed on 25 ng of reverse transcribed RNA from

each sample. 18S ribosomal RNA was measured as a control using the Pre-Developed TaqMan Assay Reagents (PDAR)(PE Applied Biosystems, CA). The assay reaction mix was as follows:

	final
TaqMan SYBR Green PCR Master Mix (2x) (PE Applied Biosystems, CA)	1x
Forward primer	300nM
Reverse primer	300nM
cDNA	25ng
Water to 25uL	

PCR conditions:

Once: 2' minutes at 50° C
10 minutes at 95°C

40cycles: 15 sec.at 95°C
1 minute at 60°C

The experiment was performed on an ABI Prism 7700 Sequence Detector (PE Applied Biosystems, CA). At the end of the run, fluorescence data acquired during PCR were processed as described in the ABI Prism 7700 user's manual. Fold change was calculated using the delta-delta CT method with normalization to the 18S values. Relative expression was calculated by normalizing to 18s (D Ct), then making the highest expressing tissue 100 and everything else relative to it. Copy number conversion was performed without normalization using the formula Cn=10(Ct-40.007)/-3.623.

The results are shown in Figs. 29 and 30.

REFERENCES

1: Tvrdik P, Westerberg R, Silve S, Asadi A, Jakobsson A, Cannon B, Loison G, Jacobsson A. Role of a new mammalian gene family in the biosynthesis of very long chain fatty acids and sphingolipids. J Cell Biol. 2000 May 1;149(3):707-18.

2: Tvrdik P, Asadi A, Kozak LP, Nedergaard J, Cannon B, Jacobsson A. Cig30, a mouse member of a novel membrane gene family, is involved in the recruitment of brown adipose tissue. J Biol Chem. 1997 Dec 12;272(50):31738-46.

3: Oh CS, Toke DA, Mandala S, Martin CE. ELO2 and ELO3, homologues of the Saccharomyces cerevisiae ELO1 gene, function in fatty acid elongation and are required for sphingolipid formation. J Biol Chem. 1997 Jul 11;272(28):17376-84.

4: Lester RL, Wells GB, Oxford G, Dickson RC. Mutant strains of Saccharomyces cerevisiae lacking sphingolipids synthesize novel inositol glycerophospholipids that mimic sphingolipid structures. J Biol Chem. 1993 Jan 15;268(2):845-56.

5: Spiegel S, Merrill AH Jr. Sphingolipid metabolism and cell growth regulation. FASEB J. 1996 Oct;10(12):1388-97. Review.

6: Simons K, Ikonen E. Functional rafts in cell membranes. Nature. 1997 Jun 5;387(6633):569-72. Review.

CLAIMS

1. An isolated polynucleotide being selected from the group consisting of:

   a) a polynucleotide encoding a elongase HSELO1-like protein polypeptide comprising an amino acid sequence selected form the group consisting of:

      amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 2 ;
      the amino acid sequence shown in SEQ ID NO: 2;
      amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NO: 4 and ;
      the amino acid sequence shown in SEQ ID NO:4;

   b) a polynucleotide comprising the sequence of SEQ ID NO: 1 or 5;

   c) a polynucleotide which hybridizes under stringent conditions to a polynucleotide specified in (a) and (b) and encodes a elongase HSELO1-like protein polypeptide;

   d) a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a elongase HSELO1-like protein polypeptide; and

   e) a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d) and encodes a elongase HSELO1-like protein polypeptide.

2. An expression vector containing any polynucleotide of claim 1.

3. A host cell containing the expression vector of claim 2.

4. A substantially purified elongase HSELO1-like protein polypeptide encoded by a polynucleotide of claim 1.

5. A method for producing a elongase HSELO1-like protein polypeptide, wherein the method comprises the following steps:

   a) culturing the host cell of claim 3 under conditions suitable for the expression of the elongase HSELO1-like protein polypeptide; and

   b) recovering the elongase HSELO1-like protein polypeptide from the host cell culture.

6. A method for detection of a polynucleotide encoding a elongase HSELO1-like protein polypeptide in a biological sample comprising the following steps:

   a) hybridizing any polynucleotide of claim 1 to a nucleic acid material of a biological sample, thereby forming a hybridization complex; and

   b) detecting said hybridization complex.

7. The method of claim 6, wherein before hybridization, the nucleic acid material of the biological sample is amplified.

8. A method for the detection of a polynucleotide of claim 1 or a elongase HSELO1-like protein polypeptide of claim 4 comprising the steps of:

contacting a biological sample with a reagent which specifically interacts with the polynucleotide or the elongase HSELO1-like protein polypeptide.

9. A diagnostic kit for conducting the method of any one of claims 6 to 8.

10. A method of screening for agents which decrease the activity of a elongase HSELO1-like protein, comprising the steps of:

contacting a test compound with any elongase HSELO1-like protein polypeptide encoded by any polynucleotide of claim1;

detecting binding of the test compound to the elongase HSELO1-like protein polypeptide, wherein a test compound which binds to the polypeptide is identified as a potential therapeutic agent for decreasing the activity of a elongase HSELO1-like protein.

11. A method of screening for agents which regulate the activity of a elongase HSELO1-like protein, comprising the steps of:

contacting a test compound with a elongase HSELO1-like protein polypeptide encoded by any polynucleotide of claim 1; and

detecting a elongase HSELO1-like protein activity of the polypeptide, wherein a test compound which increases the elongase HSELO1-like protein activity is identified as a potential therapeutic agent for increasing the activity of the elongase HSELO1-like protein, and wherein a test compound which decreases the elongase HSELO1-like protein activity of the polypeptide is identified as a potential therapeutic agent for decreasing the activity of the elongase HSELO1-like protein.

12. A method of screening for agents which decrease the activity of a elongase HSELO1-like protein, comprising the steps of:

contacting a test compound with any polynucleotide of claim 1 and detecting binding of the test compound to the polynucleotide, wherein a test compound which binds to the polynucleotide is identified as a potential therapeutic agent for decreasing the activity of elongase HSELO1-like protein.

13. A method of reducing the activity of elongase HSELO1-like protein, comprising the steps of:

contacting a cell with a reagent which specifically binds to any polynucleotide of claim 1 or any elongase HSELO1-like protein polypeptide of claim 4, whereby the activity of elongase HSELO1-like protein is reduced.

14. A reagent that modulates the activity of a elongase HSELO1-like protein polypeptide or a polynucleotide wherein said reagent is identified by the method of any of the claim 10 to 12.

15. A pharmaceutical composition, comprising:

the expression vector of claim 2 or the reagent of claim 14 and a pharmaceutically acceptable carrier.

16. Use of the expression vector of claim 2 or the reagent of claim 14 in the preparation of a medicament for modulating the activity of a elongase HSELO1-like protein in a disease.

17. Use of claim 16 wherein the disease is cancer, diabetes, CNS disorder, metabolic disease, asthma or COPD.

18. A cDNA encoding a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4.

19. The cDNA of claim 18 which comprises SEQ ID NOS:1 or 5.

20. The cDNA of claim 18 which consists of SEQ ID NOS:1 or 5.

21. An expression vector comprising a polynucleotide which encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4.

22. The expression vector of claim 21 wherein the polynucleotide consists of SEQ ID NOS:1 or 5.

23. A host cell comprising an expression vector which encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4.

24. The host cell of claim 23 wherein the polynucleotide consists of SEQ ID NOS:1 or 5.

25. A purified polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4.

26. The purified polypeptide of claim 25 which consists of the amino acid sequence shown in SEQ ID NOS:2 or 4.

27. A fusion protein comprising a polypeptide having the amino acid sequence shown in SEQ ID NOS:2 or 4.

28. A method of producing a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4, comprising the steps of:

culturing a host cell comprising an expression vector which encodes the polypeptide under conditions whereby the polypeptide is expressed; and isolating the polypeptide.

29. The method of claim 28 wherein the expression vector comprises SEQ ID NOS:1 or 5.

30. A method of detecting a coding sequence for a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4, comprising the steps of:

hybridizing a polynucleotide comprising 11 contiguous nucleotides of SEQ ID NOS:1 or 5 to nucleic acid material of a biological sample, thereby forming a hybridization complex; and detecting the hybridization complex.

31. The method of claim 30 further comprising the step of amplifying the nucleic acid material before the step of hybridizing.

32. A kit for detecting a coding sequence for a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4, comprising:

a polynucleotide comprising 11 contiguous nucleotides of SEQ ID NOS:1 or 5; and instructions for the method of claim 30.

33. A method of detecting a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4, comprising the steps of:

contacting a biological sample with a reagent that specifically binds to the polypeptide to form a reagent-polypeptide complex; and detecting the reagent-polypeptide complex.

34. The method of claim 33 wherein the reagent is an antibody.

35. A kit for detecting a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4, comprising:

an antibody which specifically binds to the polypeptide; and instructions for the method of claim 33.

36. A method of screening for agents which can modulate the activity of a human elongase HSELO1-like protein, comprising the steps of:

contacting a test compound with a polypeptide comprising an amino acid sequence selected from the group consisting of: (1) amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NOS:2or 4 and (2) the amino acid sequence shown in SEQ ID NOS:2 or 4; and

detecting binding of the test compound to the polypeptide, wherein a test compound which binds to the polypeptide is identified as a potential agent for regulating activity of the human elongase HSELO1-like protein.

37. The method of claim 36 wherein the step of contacting is in a cell.

38. The method of claim 36 wherein the cell is *in vitro*.

39. The method of claim 36 wherein the step of contacting is in a cell-free system.

40. The method of claim 36 wherein the polypeptide comprises a detectable label.

41. The method of claim 36 wherein the test compound comprises a detectable label.

42. The method of claim 36 wherein the test compound displaces a labeled ligand which is bound to the polypeptide.

43. The method of claim 36 wherein the polypeptide is bound to a solid support.

44. The method of claim 36 wherein the test compound is bound to a solid support.

45. A method of screening for agents which modulate an activity of a human elongase HSELO1-like protein, comprising the steps of:

contacting a test compound with a polypeptide comprising an amino acid sequence selected from the group consisting of: (1) amino acid sequences which are at least about 50% identical to the amino acid sequence shown in SEQ ID NOS:2 or 4 and (2) the amino acid sequence shown in SEQ ID NOS:2 or 4; and

detecting an activity of the polypeptide, wherein a test compound which increases the activity of the polypeptide is identified as a potential agent for increasing the activity of the human elongase HSELO1-like protein, and wherein a test compound which decreases the activity of the polypeptide is identified as a potential agent for decreasing the activity of the human elongase HSELO1-like protein.

46. The method of claim 45 wherein the step of contacting is in a cell.

47. The method of claim 45 wherein the cell is *in vitro*.

48. The method of claim 45 wherein the step of contacting is in a cell-free system.

49. A method of screening for agents which modulate an activity of a human elongase HSELO1-like protein, comprising the steps of:

contacting a test compound with a product encoded by a polynucleotide which comprises the nucleotide sequence shown in SEQ ID NOS:1 or 5; and

detecting binding of the test compound to the product, wherein a test compound which binds to the product is identified as a potential agent for regulating the activity of the human elongase HSELO1-like protein.

50. The method of claim 49 wherein the product is a polypeptide.

51. The method of claim 49 wherein the product is RNA.

52. A method of reducing activity of a human elongase HSELO1-like protein, comprising the step of:

contacting a cell with a reagent which specifically binds to a product encoded by a polynucleotide comprising the nucleotide sequence shown in SEQ ID NOS:1 or 5, whereby the activity of a human elongase HSELO1-like protein is reduced.

53. The method of claim 52 wherein the product is a polypeptide.

54. The method of claim 53 wherein the reagent is an antibody.

55. The method of claim 52 wherein the product is RNA.

56. The method of claim 55 wherein the reagent is an antisense oligonucleotide.

57. The method of claim 56 wherein the reagent is a ribozyme.

58. The method of claim 52 wherein the cell is *in vitro*.

59. The method of claim 52 wherein the cell is *in vivo*.

60. A pharmaceutical composition, comprising:

a reagent which specifically binds to a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4; and a pharmaceutically acceptable carrier.

61. The pharmaceutical composition of claim 60 wherein the reagent is an antibody.

62. A pharmaceutical composition, comprising:

a reagent which specifically binds to a product of a polynucleotide comprising the nucleotide sequence shown in SEQ ID NOS:1 or 5; and a pharmaceutically acceptable carrier.

63. The pharmaceutical composition of claim 62 wherein the reagent is a ribozyme.

64. The pharmaceutical composition of claim 62 wherein the reagent is an antisense oligonucleotide.

65. The pharmaceutical composition of claim 62 wherein the reagent is an antibody.

66. A pharmaceutical composition, comprising:

an expression vector encoding a polypeptide comprising the amino acid sequence shown in SEQ ID NOS:2 or 4; and a pharmaceutically acceptable carrier.

67. The pharmaceutical composition of claim 66 wherein the expression vector comprises SEQ ID NOS:1 or 5.

68. A method of treating a elongase HSELO1-like protein dysfunction related disease, wherein the disease is selected from cancer, diabetes, CNS disorders, metabolic disease, asthma or COPD comprising the step of:

administering to a patient in need thereof a therapeutically effective dose of a reagent that modulates a function of a human elongase HSELO1-like protein, whereby symptoms of the elongase HSELO1-like protein disfunction related disease are ameliorated.

69. The method of claim 68 wherein the reagent is identified by the method of claim 36.

70. The method of claim 68 wherein the reagent is identified by the method of claim 45.

71. The method of claim 68 wherein the reagent is identified by the method of claim 49.

Fig. 1

atggaa catctaaagg cctttgatga tgaaatcaat
gctttttgg acaatatgtt tggaccgcga gattctcgag tcagagggtg gttcacgttg
gactcttacc ttcctacctt ttttcttact gtcatgtatc tgctctcaat atggctgggt
aacaagtata tgaagaacag acctgctctt tctctcaggg gtatcctcac cttgtataat
cttggaatca cacttctctc cgcgtacatg ctggcagagc tcattctctc cacttgggaa
ggaggctaca acttacagtg tcaagatctt accagcgcag gggaagctga catccgggta
gccaaggtgc tttggtggta ctatttctcc aaatcagtag agttcctgga cacaattttc
ttcgttttgc ggaaaaaaac gagtcagatt acttttcttc atgtatatca tcatgcttct
atgtttaaca tctggtggtg tgtcttgaac tggatacctt gtggacaaag tttctttgga
ccaacactga acagttttgt ccacattctt atgtactcct actatggact ttctgtgttt
ccatctatgc acaagtatct ttggtggaag aaatatctca cacaggctca gctggtgcag
ttcgtgctca ccatcacgca caccatgagc gccgtcgtga aaccgtgtgg cttcccccttc
ggttgtctca tcttccagtc atcttatatg ctaacgttag tcatcctctt cttaaatttt
tatgttcaga cataccgaaa aaagccaatg aagaaagata tgcaagagcc acctgcaggg
aaagaagtga agaatggttt ttccaaagcc tacttcactg cagcaaatgg agtgatgaac
aagaaagcac aa**taa**

Fig. 2

MEHLKAFDDE INAFLDNMFG PRDSRVRGWF TLDSYLPTFF LTVMYLLSIW LGNKYMKNRP
ALSLRGILTL YNLGITLLSA YMLAELILST WEGGYNLQCQ DLTSAGEADI RVAKVLWWYY
FSKSVEFLDT IFFVLRKKTS QITFLHVYHH ASMFNIWWCV LNWIPCGQSF FGPTLNSFVH
ILMYSYYGLS VFPSMHKYLW WKKYLTQAQL VQFVLTITHT MSAVVKPCGF PFGCLIFQSS
YMLTLVILFL NFYVQTYRKK PMKKDMQEPP AGKEVKNGFS KAYFTAANGV MNKKAQ

Fig. 3

MEHLKAFDDEINAFLDNMFGPRDSRVRGWFTLDSYLPTFFLTVM
YLLSIWLGNKYMKNRPALSLRGILTLYNLGITLLSAYMLAELILSTWEGGYNLQCQDL
TSAGEADIRVAKVLWWYYFSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCV
LNWIPCGQSFFGPTLNSFVHILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTIT
HTMSAVVKPCGFPFGCLIFQSSYMLTLVILFLNFYVQTYRKKPMKKDMQEPPAGKEVK
NGFSKAYFTAANGVMNKKAQ

Fig. 4

MEHLKAFDDE INAFLDNMFG PRDSRVRGWF MLDSYLPTFF LTVMYLLSIW LGNKYMKNRP
ALSLRGILTL YNLGITLLSA YMLAELILST WEGGYNLQCQ DLTSAGEADI RVAKVLWWYY
FSKSVEFLDT IFFVLRKKTS QITFLHVYHH ASMFNIWWCV LNWIPCGQSF FGPTLNSFIH
ILMYSYYGLS VFPSMHKYLW WKKYLTQAQL VQFVLTITHT MSAVVKPCGF PFGCLIFQSS
YMLTLVILFL NFYVQTYRKK PMKKDMQEPP AGKEVKNGFS KAYFTAANGV MNKKAQ

Fig. 5

atggaa catctaaagg cctttgatga tgaaatcaat
gctttttgg acaatatgtt tggaccgcga gattctcgag tcagagggtg gttcatgttg
gactcttacc ttcctacctt ttttcttact gtcatgtatc tgctctcaat atggctgggt
aacaagtata tgaagaacag acctgctctt tctctcaggg gtatcctcac cttgtataat
cttggaatca cacttctctc cgcgtacatg ctggcagagc tcattctctc cacttgggaa
ggaggctaca acttacagtg tcaagatctt accagcgcag gggaagctga catccgggta
gccaaggtgc tttggtggta ctatttctcc aaatcagtag agttcctgga cacaattttc
ttcgttttgc ggaaaaaaac gagtcagatt acttttcttc atgtatatca tcatgcttct
atgtttaaca tctggtggtg tgtcttgaac tggatacctt gtggacaaag tttctttgga
ccaacactga acagttttat ccacattctt atgtactcct actatggact ttctgtgttt
ccatctatgc acaagtatct ttggtggaag aaatatctca cacaggctca gctggtgcag
ttcgtgctca ccatcacgca caccatgagc gccgtcgtga aaccgtgtgg cttcccttc
ggttgtctca tcttccagtc atcttatatg ctaacgttag tcatcctctt cttaaatttt
tatgttcaga cataccgaaa aaagccaatg aagaaagata tgcaagagcc acctgcaggg
aaagaagtga agaatggttt ttccaaagcc tacttcactg cagcaaatgg agtgatgaac
aagaaagcac aa**taa**

Fig. 6

gatagcgccg ggcagaggga cccggctacc ctggacagcg catcgccgcc cgcccgggtc
gccgcgccac agccgctgcg gatc**atg**gaa catctaaagg cctttgatga tgaaatcaat
gctttttgg acaatatgtt tggaccgcga gattctcgag tcagagggtg gttcacgttg
gactcttacc ttcctacctt ttttcttact gtcatgtatc tgctctcaat atggctgggt
aacaagtata tgaagaacag acctgctctt tctctcaggg gtatcctcac cttgtataat
cttggaatca cacttctctc cgcgtacatg ctggcagagc tcattctctc cacttgggaa
ggaggctaca acttacagtg tcaagatctt accagcgcag gggaagctga catccgggta
gccaaggtgc tttggtggta ctatttctcc aaatcagtag agttcctgga cacaattttc
ttcgttttgc ggaaaaaaac gagtcagatt acttttcttc atgtatatca tcatgcttct
atgtttaaca tctggtggtg tgtcttgaac tggatacctt gtggacaaag tttctttgga
ccaacactga acagttttgt ccacattctt atgtactcct actatggact ttctgtgttt
ccatctatgc acaagtatct ttggtggaag aaatatctca cacaggctca gctggtgcag
ttcgtgctca ccatcacgca caccatgagc gccgtcgtga aaccgtgtgg cttcccttc
ggttgtctca tcttccagtc atcttatatg ctaacgttag tcatcctctt cttaaatttt
tatgttcaga cataccgaaa aaagccaatg aagaaagata tgcaagagcc acctgcaggg
aaagaagtga agaatggttt ttccaaagcc tacttcactg cagcaaatgg agtgatgaac
aagaaagcac aa**taa**aaaatg agtaacagaa aaagcacata tactagccta acagattggc
ttgttttaaa gcaaagactg aattgaaggt tacatgtttt aggataaact aatttctttt
gagttcataa atcatttgta cccagaatgt attaatatat tgctattagg ttaatctgtt
aactgaatgc tttgatcagc attgaggtga tgctcacctc cgaggacctc agaactggtg
cagcttctct ctccctccct cccacagact gaacctttcg ccagaagctg tccttataac
gccttatacg catacacagc caggaaacgt ggagcattgt ttctcacaga gagtctccaa
ataaaaaggg ttttgttcag attaaaatgt ttacaacaaa atgttaatta tattctaaat
acagggtatg ttctaatcta tattaagcaa taatgccagt gcataatcat tccatttgtt

Fig. 6 (continued)

cctttagcaa tcaaccccag aaaatattaa aatgggatca tacacagaag atagaaaaat
ctagcaaaac ttctctttct gtaagccaga gtcttgtcta tcagattccc acaaccactc
ctgattctaa atttagtgat atggtaatga aattggtatt tattttaaat attagttatt
ctaaggagaa aaaaatgctt ctgcaagatt ttcataattc aggggctgtg gataggattg
ttcctctgtt tccctaatca ttcatctgtt catgtctccc tcttgtgcca gtcagcctag
gttatacaga tgccatgctc cacaccacga gcagtgtaca aatctggctg cccgtttact
ttctgagcaa gcactggagt ccactccgac ctttttcttt gaacatgcat gctgctggaa
tatgtataaa tcagaactag cagaagtagc agagtgatgg gagcaaaata ggcactgaat
tcgtcaactc ttttttgtga gcctacttgt gaatattacc tcagatacct gttgtcactc
ttcacaggtt atttaagttc ttgaagctgg gaggaaaaag atggagtagc ttggaaagat
tccagcactg agccgtgagc cggtcatgag ccacgataaa aaatgccagt ttggcaaact
cagcactcct gttccctgct caggtatatg cgatctctac tgagaagcaa gcacaaaagt
agaccaaagt attaatgagt atttcctttc tccataagtg caggactgtt actcactact
aaactctacc aagaatggaa accaagaata ttttctgaag attttttttga agattaattt
ataccctata aaataaaact tgttagcttc gatgaagtca aaaaaaaaaa aaaaaaaaaa

Fig. 7

gatagcgccg ggcagaggga cccggctacc ctggacagcg catcgccgcc cgcccgggtc
gccgcgccac agccgctgcg gatc**atg**gaa catctaaagg cctttgatga tgaaatcaat
gctttttttgg acaatatgtt tggaccgcga gattctcgag tcagagggtg gttcatgttg
gactcttacc ttcctacctt ttttcttact gtcatgtatc tgctctcaat atggctgggt
aacaagtata tgaagaacag acctgctctt tctctcaggg gtatcctcac cttgtataat
cttggaatca cacttctctc cgcgtacatg ctggcagagc tcattctctc cacttgggaa
ggaggctaca acttacagtg tcaagatctt accagcgcag gggaagctga catccgggta
gccaaggtgc tttggtggta ctatttctcc aaatcagtag agttcctgga cacaattttc
ttcgttttgc ggaaaaaaac gagtcagatt acttttcttc atgtatatca tcatgcttct
atgtttaaca tctggtggtg tgtcttgaac tggatacctt gtggacaaag tttctttgga
ccaacactga acagttttat ccacattctt atgtactcct actatggact ttctgtgttt
ccatctatgc acaagtatct ttggtggaag aaatatctca cacaggctca gctggtgcag
ttcgtgctca ccatcacgca caccatgagc gccgtcgtga aaccgtgtgg cttccccttc
ggttgtctca tcttccagtc atcttatatg ctaacgttag tcatcctctt cttaaatttt
tatgttcaga cataccgaaa aaagccaatg aagaaagata tgcaagagcc acctgcaggg
aaagaagtga agaatggttt ttccaaagcc tacttcactg cagcaaatgg agtgatgaac
aagaaagcac aa**taa**aaatg agtaacagaa aaagcacata tactagccta acagattggc
ttgttttaaa gcaaagactg aattgaaggt tacatgtttt aggataaact aatttctttt
gagttcataa atcatttgta cccagaatgt attaatatat tgctattagg ttaatctgtt
aactgaatgc tttgatcagc attgaggtga tgctcacctc cgaggacctc agaactggtg
cagcttctct ctccctccct cccacagact gaacctttcg ccagaagctg tccttataac
gccttatacg catacacagc caggaaacgt ggagcattgt ttctcacaga gagtctccaa
ataaaaaggg ttttgttcag attaaaatgt ttacaacaaa atgttaatta tattctaaat
acagggtatg ttctaatcta tattaagcaa taatgccagt gcataatcat tccatttgtt
cctttagcaa tcaaccccag aaaatattaa aatgggatca tacacagaag atagaaaaat

Fig. 7 (continued)

ctagcaaaac ttctctttct gtaagccaga gtcttgtcta tcagattccc acaaccactc
ctgattctaa atttagtgat atggtaatga aattggtatt tattttaaat attagttatt
ctaaggagaa aaaaatgctt ctgcaagatt ttcataattc aggggctgtg gataggattg
ttcctctgtt tccctaatca ttcatctgtt catgtctccc tcttgtgcca gtcagcctag
gttatacaga tgccatgctc cacaccacga gcagtgtaca aatctggctg cccgtttact
ttctgagcaa gcactggagt ccactccgac ctttttcttt gaacatgcat gctgctggaa
tatgtataaa tcagaactag cagaagtagc agagtgatgg gagcaaaata ggcactgaat
tcgtcaactc ttttttgtga gcctacttgt gaatattacc tcagatacct gttgtcactc
ttcacaggtt atttaagttc ttgaagctgg gaggaaaaag atggagtagc ttggaaagat
tccagcactg agccgtgagc cggtcatgag ccacgataaa aaatgccagt ttggcaaact
cagcactcct gttccctgct caggtatatg cgatctctac tgagaagcaa gcacaaaagt
agaccaaagt attaatgagt atttcctttc tccataagtg caggactgtt actcactact
aaactctacc aagaatggaa accaagaata ttttctgaag attttttttga agattaattt
ataccctata aaataaaact tgttagcttc gatgaagtca aaaaaaaaaa aaaaaaaaaa

Fig. 8

AGCGCCGGGCAGAGGGACCCGGCTACCCTGGACAGCGCATCGCCGTCCGCCCGGGTCGCC
GCGCCACAGCCGCTGCGGATCATGGAACATCTAAAGGCCTTTGATGATGAAATCAATTGC
TTTTTTGGACAATATGTTTGGACCGCGAGATTCTCGAGTCAGAGGGTGGTTCATGTTGGA
CTCTTACCTTCCTACCTTTTTTCTTACTGTCATGTATCTGCTCTCAATATGGCTGGGTAA
CAAGTATATGAAGAACAGACCTGCTCTTTCTCTCAGGGGTATCCTCACCTTGTATAATCT
TGGAATCACACTTCTCTCCGCGTACATGCTGGCAGAGCTCATTCTCTCCACTTGGGAAGG
AGGCTACAAGCTTACAGTGTCAAGATCTTACCAGCGCAGGGGAAGCTGACATCCGGGTAG
CCAAGGTGCTTCGGTGGTACTATTTCTCCAAATCAGTAGAGTTCCTGGACACAATTTTCT
TCGTTTTGCGGAAAAAAACGAGTCAGATTACTTTTCTTCATGTATATCATCATGCTTCTA
TGTTTAACATCTGGTGGTGTGTCTTGAACTGGATACCTGGTGGACAAAGTTTCTTTGGAC
CAACACTGAACAGTTTTATCCACATTCTTATGTACTCCTACTATGGACCTTTCTGGTGTT
TCCATTTTATGCGCCACGTATCTTCGGGGGGAACAAACTTTTCCCACCAGTGCTCCGACT
GGTGCCGTCGGGGGCACCCATAAGGCGAACCATGAGGCCGTCGGAACCCGGGTGGTTCCC
TTTGGGGTGTCAATATCCGGACAGTATATGTACAGAGTGAGAACAGTATAATGGTGTGTT
ATCGTGGTGCTAATCGGAAAAGGACGTGACGAAAGGATGCTAGCAATACTGGCGATCAGC
TAGAAGTGGTGTCCCACCATGCGGCAGGCAGTGCTGACAATGACAACGGAGAGTGAAGAG
CATATACGAATGATTGTAGTAGCAGGAAGACTGCGAGCGAAAGATGACGACATTGGACGA
AACTGGTAAGACGTACGAGGGCACACAGTGTCTTGCTTCACCGTCCCTTCTTCTTCCTCG
TGTTCGCN

Fig. 9

CCTTGTATAATCTTGGAATCACACTTCTCTCCGCGTACATGCTGGCAGAGCTCATTCTCT
CCACTTGGGAAGGAGGCTACAACTTACAGTGTCAAGATCTTACCAGCGCAGGGGAAGCTG
ACATCCGGGTAGCCAAGGTGCTTTGGTGGTACTATTTCTCCAAATCAGTAGAGTTCCTGG
ACACAATTTTCTTCGTTTTGCGGAAAAAAACGAGTCAGATTACTTTTCTTCATGTATATC
ATCATGCTTCTATGTTTAACATCTGGTGGTGTGTCTTGAACTGGATACCTTGTGGACAAA
GTTTCTTTGGACCAACACTGAACAGTTTTATCCACATTCTTATGTACTCCTACTATGGAC
TTTCTGTGTTTCCATCTATGCACAAGTATCTTTGGTGGAAGAAATATCTCACACAGGCTC
AGCTGGTGCAGTTCG

Fig. 10

GGTAGAGTTTAGTAGTGAGTAACAGTCCTGCACTTATGGAGAAAGGAAATACTCATTAAT
ACTTTTGTCTACTTTTGTGCTTGCTTCTCAGTAGAGATCGCATATACCTGAGCAGGGAAC
AGGAGTGCTGAGTTTGCCAAACTGGCATTTTTTATCGTGGCTCATGACCGGCCCACGGCT
CAGTGCTGGAATCTTTCCAAGCTACTCCATCTTTTTCCTCCCAGCTTCAAAAACTTAAAT
AACCTGTGAAGAGTGACAACAGGTATCTGAGGTAATATTCACAAGTAGGCTCACAAAAAA
GAGTTGACGAATTCAGTGCCTATTTTGCTCCCATCACTCTGCTACTTCTGCTAGTTCTGA
TTTATACATATTCCAGCAGCATGCATGTTCAAAGAAAAAGGTCGGAGTGGACTCCAGTGC
T

Fig. 11

TTTTAATCTGAACAAAACCCTTTTTATTTGGAGACTCTCTGTGAGAAACAATGCTCCACG
TTTCCTGGCTGTGTATGCGTATAAGGCGTTATAAGGACAGCTTCTGGCGAAAGGTTCAGT
CTGTGGGAGGGAGGGAGAGAGAAGCTGCACCAGTTCTGAGGTCCTCGGAGGTGAGCATCA
CCTCAATGCTGATCAAAGCATTCAGTTAACAGATTAACCTAATAGCAATATATTAATACA
TTCTGGGTACAAATGATTTATGAACTCAAAAGAAATTAGTTTATCCTAAAACATGTAACC
TTCAATTCAGTCTTTGCTTTAAAACAAGCCAATCTGTTAGGCTAGTATATGTGCTTTTTC
TGTTACTCATTTTTATTGTGCTTTCTTGTTCATCACT

Fig. 12

TGANCCTTTCGCCAGANGCTGTCCTTATAACGCCTTATACGCATACACAGCCAGGAAACG
TGGAGCATTGTTTCTNACAGAGAGTCTCCAAATAAAAAGGGTTTTGTTCANATTAAANTG
TTTACAACAAAATGTTAATTATATTCTAAATACAGGGTATGTTCTAATCTATATTAAGCA
ATAATGCCAGTGCATAATCATTCCATTTGTTCCTTTAGCAATCAACCCCAGAAAATATTA
AAATGGGNTCATACACAGAAGATAGAAACATCTAGCAAAACTTCTCTTTCTGTAAGCCAG
AGTCTTGTCTATCAGATTCCCACAACCACTCCTGATTCTAAAATTTAGTGGATATGGGTA

Fig. 13

GGGAAGCTGACATCCGGGTAGCCAAGGTGCTTTGGTGGTACTATTTCTCCAAATCAGTAG
AGTTCCTGGACACAATTTTCTTCGTTTTGCGGAAAAAAACGAGTCAGATTACTTTTCTTC
ATGTATATCATCATGCTTCTATGTTTAACATCTGGTGGTGTGTCTTGAACTGGATACCTT
GTGGACAAAGTTTCTTTGGACCAACACTGAACAGTTTTATCCACATTCTTATGTACTC

Fig. 14

GAGTACATAAGAATGTGGATAAAACTGTTCAGTGTTGGTCCAAAGAAACTTTGTCCACAA
GGTATCCAGTTCAAGACACACCACCAGATGTTAAACATAGAAGCATGATGATATACATGA
AGAAAGGTAATCTGACTCGTTTTTTTCCGCAAAACGAAGAAAATTGTGTCCAGGAACTCT
ACTGATTTGGAGAAATAGTACCACCAAAGCACCTTGG

Fig. 15

CGATCTCTACTGAGAAGCAAGCACAAAAGTAGACAAAAGTATTAATGAGTATTTCCTTTC
TCCATAAGTGCAGGACTGTTACTCACTACTAAACTCTACCAAGAATGGAAACAAAGAATA
TTTTCTGAAGATTTTTTTGAAGATTAATTTATACCCTATAAAATAAAACTTGTTAGCTTC
GATGAAGTCACTTCATCTTCTCTCCTACCTTATTTTTTTAAATAAGTTTTTAGGTCCTGA
CACTGACATCAAATACATGCACACCAGAAAGGCATTTCCACCACCGTCCCCACTCATTAG
CGTCCAGAGTGCCTTTCTCTCTCGGCTTTTTTTCCCCCCTGAGCTCTAGTTTTAAACTTT
CTCCTGTTAAAAAAATTGTACTTTTATTTCATGTAAACTGCCCCNCTGGAGGGNTTGGGG
CNTATTTTTTGGGAAGGTGCCNAATGCTTAGGGTAGTCTCTAGGGTGATGCACTGCACCT
GCTTCCTTCCCTTCAGTGCGGGNCGACCATTTCNGTTGAACAGATGTCTCCGGN

Fig. 16

CCTTGTATAATCTTGGAATCACACTTCTCTCCGCGTACATGCTGGCAGAGCTCATTCTCT
CCACTTGGGAAGGAGGCTACAACTTACAGTGTCAAGATCTTACCAGCGCAGGGGAAGCTG
ACATCCGGGTAGCCAAGGTGCTTTGGTGGTACTATTTCTCCAAATCAGTAGAGTTCCTGG
ACACAATTTTCTTCGTTTTGCGGAAAAAAACGAGTCAGATTACTTTTCTTCATGTATATC
ATCATGCTTCTATGTTTAACATCTGGTGGTGTGTCTTGAACTGGATACCTTGTGGACAAA
GTTTCTTTGGACCAACACTGAACAGTTTTATCCACATTCTTATGTACTCCTACTATGGAC
TTTCTGTGTTTCCATCTATGCACAAGTATCTTTGGTGGAAGAAATATCTCACACAGGCTC
AGCTGGTGCAGTTCG

Fig. 17

cggctaccct ggacagcgca tcgcggccgc gcggccatgg agcagctgaa ggcctttgat
aatgaagtca atgctttctt ggacaacatg tttggaccac gagattctcg agttcgcggg
tggttcctgc tggactctta ccttcccacc ttcatcctca ccatcacgta cctgctctcg
atatggctgg gtaacaagta catgaagaac aggcctgctc tgtctctcag gggcatcctc
accttgtata acctcgcaat cacacttctt tctgcgtata tgctggtgga gctcatcctc
tccagctggg aaggaggtta caacttgcag tgtcagaatc tcgacagtgc aggagaaggt
gatgtccggg tagccaaggt cttgtggtgg tactacttct ccaaactagt ggagttcctg
gacacgattt tctttgttct acgaaaaaag accaatcaga tcaccttcct tcatgtctat
caccacgcgt ccatgttcaa catctggtgg tgtgttttga actggatacc ttgtggtcaa
agcttctttg gacccaccct gaacagcttt atccacattc tcatgtactc ctactacggc
ctgtctgtgt tcccgtccat gcacaagtac ctttggtgga agaagtacct cacacaggct
cagctggtgc agttcgtact caccatcacg cacacgctga gtgccgtggt gaagccctgt
ggcttcccct ttggctgtct catcttccag tcttcctata tgatgacgct ggtcatcctg
ttcttaaact tctatattca gacataccgg aaaaagccag tgaagaaaga gctgcaagag
aaagaagtga agaatggttt ccccaaagcc cacttaattg tggctaatgg catgacggac
aagaaggctc aataaaatga agtgccgggg aacacaaact gaggtggtgg cggcggcggc
ggcggcagca aacagacgag cttgttttaa agcagagact gaatagaaag ttgtatgttt
tagcataaac taattccttt tgagtttgta aatcatttgt acccagaatg tattataata
tattgctatt aggttactct actaactgga gccatgccga cctctacaaa ccttgaacag
gtgcacagcc ccctctccgg agcgctttgt aatgccttat tcacgtcgaa aaccaggaga
ctcgggcttc gtttcttcat ggcaagtctt cagagttaat tttctttaga tgtgtaaaac
tgttcattgt agtgtaaatg tcagggtctg ttctagtcta tgtcaagcaa taactgtcag
tgcataaatc gattagtctg ctgttgctta aggcagcagc cccaggcagc atttaagcgg
gatccttagc aagacagaat ccagcaaaac cctttcccct ctcaagccag gagtctcatc
tgctacattt tttttaacca cctctgattt ccaacttagt gatgtggtaa tgaaattcgt

Fig. 17 (continued)

ttgtcttcaa tatagtttga agattagtca ttccatgaag gaacagcctc ttgagctggg
tatggtggca cccatctgtg agtccagcat ttgggtattg agacagccta gggtacacag
gcacaagacc ctgtctcaac cagaaaagaa aaatgtgttt gccaaatcat aactcagggg
ctttgaacag agctgtctct gtttcaattg gcatccttgc tcatccattc ctgtctacct
cccttgttag tctagatttc tggagttatg ttccccacat ccaaagccag tgtctacata
cagctgccat gccctttctg aacaaaggct ggagttgtcc aattgcagtt cttcttcgca
tagaaatgca attggaatat ttacaaatca taatcaacag agccccaggg gcaaaataga
cattctattt gtcagctgtt gctgctgagc ctgctggtga acaccattgc aagcagttgc
tgagcctgct ggtgaacacc attgcaagca gttgctgagc ctgctcgtga acaccattgc
aagccattgc tgtcaagctt catgagttaa atttaactgt tagagaggag aaaagcatag
cagtcatttg gaacgatctc gtggggtggg actaagccat aatgatgtgt ctggctcaag
cagcaatgct gtccctgctc agaactgtgg tctctgtgga gaacctagta cagagcctga
gcaaggcaat ggaccacctc cttttcctca aactgatgga tcaccactgt taatctatac
caggtgtgaa aaagggcatt tcccaaaaca tacacaaaac acaacttact ctatttcccc
tccatttcag caaatgtgtt cttggttcat ggcactggca cccagcgcat gggcaccagg
taggtgttcc tcgagtgcca acggcggggc ctgccacccc tgcttccttt ctgggcaagc
tcccatttta acttttccct gttaaaaatt gtactgatgt tttaaactcg taactatacc
acccttctca ctggtgtatt ttgaaaacca ccacagtccg atgtcctgtg ccatgtctgt
cattcctgtt gaacagactc ttcctgtctg gtgaccacct atgcttcagt gcattttcta
aacaatttct caaactgatc tgctcccggg tgctttctta ccaccatctc tggtgactta
gcctcaaatt ggtgtttttc tttcccaaga attcatctta agggttagct ttgagtatgt
tactgtcctt ctatgacaag accaaaggaa caaactcctt ggtgaatctg gagttcagct
ttagttttca aacacaatct gaaatctgtt agtaaaatga attctgggta aaaatgagac
tcaagaggca tcactggcca ttgtaccaga ttattcctgc tcgccagtga gaggcgttta
agtcgcgctg tgcatcgtac cttcagttta ggctgttttc atgacctcac atctgtgtag

Fig. 17 (continued)

```
cacaaagggt gttatcttcc tatagcagat caacagtggc agctcacagt accagccagc
tttagacctc ccagtgcaaa gcccagcgca gcactaagcc ttaagccacc caagggctga
cacaccatgc agagctacga aatctgtgct gagaaaatgc catctggaaa gatttttaac
ccattcattc ttagtgtgaa ttttctaaaa tagaagtata aaaaaaaagt ctctataatc
tgataggaaa ccgtcttttc ccaagtgaat tccctttttat tcatgagaac aaaagtactt
agatactata aaaccttaat ttccccaact tttaaaataa aatggaatat ttgctgaatg
aattaagcat agaaaatgtc aacccatcag aattatattt atacatattg gtggataagt
tcttgtcttc ccacatcaga gaatttttttt ttaaaccaaa atgggcagaa tagcattttg
tatgttagag accattcttt tctagtcctt ccaaacattc ctgtgtcact taagaatgtt
agtagaggtc gcttctttgg aaattgagga ctttttttttt tcctttgaaa gtatggcatc
tgaagaacac agtatcatga ctcgggtgga aagggaggca gaagccattt ttcttttaga
tgaaaagcat tctgtgtgat tgttgtataa taaattgatt tttacact
```


Fig. 18

```
MEHFDASLSTYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLL
IVWLGPKYMRNKQPFSCRGILVVYNLGLTLLSLYMFCELVTGVWEGKYNFFCQGTRTA
GESDMKIIRVLWWYYFSKLIEFMDTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNW
VPCGHSYFGATLNSFIHVLMYSYYGLSSVPSMRPYLWWKKYITQGQLLQFVLTIIQTS
CGVIWPCTFPLGWLYFQIGYMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAA
VNGHTNSFSPLENNVKPRKLRKD
```


Fig. 19

```
mnslvtqyaa plferypqlh dylptlerpf fnislwehfd dvvtrvtngr fvpsefqfia
gelplstlpp vlyaitayyv iifggrflls kskpfklngl fqlhnlvlts lsltllllmv
eqlvpiivqh glyfaicnig awtqplvtly ymnyivkfie fidtfflvlk hkkltflhty
hhgatallcy tqlmgttsis wvpislnlgv hvvmywyyfl aargirvwwk ewvtrfqiiq
fvldigfiyf avyqkavhly fpilphcgdc vgsttatfag caiissylvl fisfyinvyk
rkgtktsrvv krahggvaak vneyvnvdlk nvptpspspk pqhrrkr
```

Fig. 20

```
mntttstvia avadqfqsln sssscflkvh vpsienpfgi elwpifskvf eyfsgypaeq
fefihnktfl angyhavsii ivyyiiifgg qailralnas plkfkllfei hnlfltsisl
vlwllmleql vpmvyhnglf wsicskeafa pklvtlyyln yltkfvelid tvflvlrrkk
llflhtyhhg atallcytql igrtsvewvv illnlgvhvi mywyyflssc girvwwkqwv
trfqiiqfli dlvfvyfaty tfyahkyldg ilpnkgtcyg tqaaaaygyl iltsylllfi
sfyiqsykkg gkktvkkese vsgsvasgss tgvktsntkv ssrka
```

Fig. 21

BLASTP - alignment of 391_protein_modified against trembl|AK000341|AK000341_1
unnamed ORF; Homo sapiens cDNA FLJ20334 fis, clone HEP11362. //:gp|AK000341|7020361
unnamed ORF; Homo sapiens cDNA FLJ20334 fis, clone HEP11362.

This hit is scoring at : 5e-178 (expectation value)
Alignment length (overlap) : 296
Identities : 99 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:      1 MEHLKAFDDEINAFLDNMFGPRDSRVRGWFMLDSYLPTFFLTVMYLLSIWLGNKYMKNRP
          MEHLKAFDDEINAFLDNMFGPRDSRVRGWF.LDSYLPTFFLTVMYLLSIWLGNKYMKNRP
H:      1 MEHLKAFDDEINAFLDNMFGPRDSRVRGWFTLDSYLPTFFLTVMYLLSIWLGNKYMKNRP

          ALSLRGILTLYNLGITLLSAYMLAELILSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYY
          ALSLRGILTLYNLGITLLSAYMLAELILSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYY
          ALSLRGILTLYNLGITLLSAYMLAELILSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYY

          FSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFIH
          FSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSF:H
          FSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFVH

          ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHTMSAVVKPCGFPFGCLIFQSS
          ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHTMSAVVKPCGFPFGCLIFQSS
          ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHTMSAVVKPCGFPFGCLIFQSS
```

Fig. 21 (continued)

```
          YMLTLVILFLNFYVQTYRKKPMKKDMQEPPAGKEVKNGFSKAYFTAANGVMNKKAQ     296
          YMLTLVILFLNFYVQTYRKKPMKKDMQEPPAGKEVKNGFSKAYFTAANGVMNKKAQ
          YMLTLVILFLNFYVQTYRKKPMKKDMQEPPAGKEVKNGFSKAYFTAANGVMNKKAQ     296
```

Fig. 22

```
BLASTP - alignment of 391_protein_modified against trembl|AF170908|AF170908_1
 gene: "Ssc2"; product: "SSC2"; Mus musculus SSC2 (Ssc2) mRNA, complete cds.
 //:gp|AF170908|8101521 gene: "Ssc2"; product: "SSC2"; Mus musculus SSC2 (Ssc2)
mRNA,
 complete cds.

 This hit is scoring at : 5e-159 (expectation value)
 Alignment length (overlap) : 296
 Identities : 88 %
 Scoring matrix : BLOSUM62 (used to infer consensus pattern)
 Database searched : nrdb_1_;

 Q:       1 MEHLKAFDDEINAFLDNMFGPRDSRVRGWFMLDSYLPTFFLTVMYLLSIWLGNKYMKNRP
             ME.LKAFD:E:NAFLDNMFGPRDSRVRGWF:LDSYLPTF.LT:.YLLSIWLGNKYMKNRP
 H:       1 MEQLKAFDNEVNAFLDNMFGPRDSRVRGWFLLDSYLPTFILTITYLLSIWLGNKYMKNRP

             ALSLRGILTLYNLGITLLSAYMLAELILSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYY
             ALSLRGILTLYNL.ITLLSAYML.ELILS:WEGGYNLQCQ:L.SAGE.D:RVAKVLWWYY
             ALSLRGILTLYNLAITLLSAYMLVELILSSWEGGYNLQCQNLDSAGEGDVRVAKVLWWYY

             FSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFIH
             FSK VEFLDTIFFVLRKKT:QITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFIH
             FSKLVEFLDTIFFVLRKKTNQITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFIH
```


Fig. 22 (continued)

```
             ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHTMSAVVKPCGFPFGCLIFQSS
             ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHT:SAVVKPCGFPFGCLIFQSS
             ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHTLSAVVKPCGFPFGCLIFQSS

      YMLTLVILFLNFYVQTYRKKPMKKDMQEPPAGKEVKNGFSKAYFTAANGVMNKKAQ      296
      YM:TLVILFLNFY:QTYRKKP:KK::QE     KEVKNGF.KA:...ANG:.:KKAQ
      YMMTLVILFLNFYIQTYRKKPVKKELQE----KEVKNGFPKAHLIVANGMTDKKAQ      292
```

Fig. 23

```
BLASTP - alignment of 391_protein_modified against aageneseq|Y83932|Y83932
 Human elongase HSELO1.

 This hit is scoring at : 5e-103 (expectation value)
 Alignment length (overlap) : 298
 Identities : 56 %
 Scoring matrix : BLOSUM62 (used to infer consensus pattern)
 Database searched : aageneseq

 Q:       1 MEHLKAFDDEINAFLDNMFGPRDSRVRGWFMLDSYLPTFFLTVMYLLSIWLGNKYMKNRP
             MEH    FD .::.:.. :.GPRD:RV:GWF:LD:Y:PTF..:V:YLL :WLG KYM:N:.
 H:       1 MEH---FDASLSTYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQ

             ALSLRGILTLYNLGITLLSAYMLAELILSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYY
             ..S.RGIL.:YNLG:TLLS.YM..EL:...WEG YN. CQ...:AGE:D::::VLWWYY
             PFSCRGILVVYNLGLTLLSLYMFCELVTGVWEGKYNFFCQGTRTAGESDMKIIRVLWWYY

             FSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFIH
             FSK :EF:DT.FF:LRK...QIT.LHVYHHASM.NIWW V:NW:PCG.S:FG.TLNSFIH
             FSKLIEFMDTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNWVPCGHSYFGATLNSFIH

             ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHTMSAVVKPCGFPFGCLIFQSS
             :LMYSYYGLS .PSM..YLWWKKY:TQ.QL:QFVLTI..T...V: PC FP.G L.FQ .
             VLMYSYYGLSSVPSMRPYLWWKKYITQGQLLQFVLTIIQTSCGVIWPCTFPLGWLYFQIG
```

Fig. 23 (continued)

```
YMLTLVILFLNFYVQTYRKK--PMKKD--MQEPPAGKEVKNGFSKAYFTAANGVMNKK      294
YM::L:.LF.NFY:QTY.KK  ..:KD  .... ..... NG.:.:: ...N.V. :K
YMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNVKPRK      295
```

Fig. 24

BLASTP - alignment of 391_protein_modified against tremblnew|AL136939|HSM801903_1
gene: "DKFZp586B1824"; product: "hypothetical protein"; Homo sapiens mRNA; cDNA
DKFZp586B1824 (from clone DKFZp586B1824); complete cds
//:trembl|AF231981|AF231981_1 gene: "HELO1"; product: "long chain polyunsaturated
fatty acid elongation enzyme";
Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA,
complete cds. //:gp|AF231981|7920390 gene: "HELO1"; product: "long chain
polyunsaturated fatty acid elongation e nzyme"; Homo sapiens long chain
polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds.
//:gpnew|AL136939|12053373 gene:
"DKFZp586B1824"; product: "hypothetical protein"; Homo sapiens mRNA; cDNA
DKFZp586B1824 (from clone DKFZp586B1824); complete cds.

This hit is scoring at : 5e-102 (expectation value)
Alignment length (overlap) : 298
Identities : 56 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:      1 MEHLKAFDDEINAFLDNMFGPRDSRVRGWFMLDSYLPTFFLTVMYLLSIWLGNKYMKNRP
            MEH   FD .:.:.:. :.GPRD:RV:GWF:LD:Y:PTF..:V:YLL :WLG KYM:N:.
H:      1 MEH---FDASLSTYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQ

          ALSLRGILTLYNLGITLLSAYMLAELILSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYY
          ..S.RGIL.:YNLG:TLLS.YM..EL:...WEG YN. CQ...:AGE:D::::VLWWYY
          PFSCRGILVVYNLGLTLLSLYMFCELVTGVWEGKYNFFCQGTRTAGESDMKIIRVLWWYY
```


Fig. 24 (continued)

```
          FSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFIH
          FSK :EF:DT.FF:LRK...QIT.LHVYHHASM.NIWW V:NW:PCG.S:FG.TLNSFIH
          FSKLIEFMDTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNWVPCGHSYFGATLNSFIH

          ILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTITHTMSAVVKPCGFPFGCLIFQSS
          :LMYSYYGLS .PSM..YLWWKKY:TQ.QL:QFVLTI..T...V: PC FP.G L.FQ .
          VLMYSYYGLSSVPSMRPYLWWKKYITQGQLLQFVLTIIQTSCGVIWPCTFPLGWLYFQIG

YMLTLVILFLNFYVQTYRKK--PMKKD--MQEPPAGKEVKNGFSKAYFTAANGVMNKK     294
YM::L:.LF.NFY:QTY.KK  ..:KD  .... ..... NG.:.:: ...N.V. :K
YMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNVKPRK     295
```

Fig. 25

BLASTP - alignment of 391_protein_modified against swiss|P25358|GNS1_YEAST
GNS1 PROTEIN.//:trembl|AF012655|AF012655_1 gene: "VBM2"; product: "v-SNARE bypass mutant"; Saccharomyces cerevisiae v-SNARE bypass mutant (VBM2) gene, complete cds. //:trembl|S78624|S78624_3 gene: "YCR521"; YCR591...YCR522 [Saccharomyces cerevisiae=yeast, Genomic, 4 genes, 7532 nt]. //:trembl|X59720|SCCHRIII_102 gene: "GNS1"; S.cerevisiae
chromosome III complete DNA sequence //:trembl|X56909|SCSMAT_1 gene: "YCR521"; S.cerevisiae 8.2 kb segment left of MAT /:gp|AF012655|2654761 gene: "VBM2"; product: "v-SNARE bypass mutant"; Saccharomyces cerevisiae v-SNARE bypass mutant (VBM2) gene, complete cds. //:gp|S78624|244240 gene: "YCR521"; YCR591...YCR522 [Saccharomyces
cerevisiae=yeast, Genomic, 4 genes, 7532 nt]. //:gp|X59720|1907176 gene: "GNS1"; S.cerevisiae chromosome III complete DNA sequence. //:gp|X56909|4490 gene: "YCR521"; S.cerevisiae 8.2 kb segment left of MAT.

This hit is scoring at : 6e-20 (expectation value)
Alignment length (overlap) : 288
Identities : 27 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:       7 FDDEINAFLDNMFGPRDSR-VRGWFMLDSYLPTFFLTVMYLLSIWLGNKYMKNRPALSLR
           FDD :....:..F P.: : :.G . L.:. P..:....Y.: I: G. .:.......L.
H:      39 FDDVVTRVTNGRFVPSEFQFIAGELPLSTLPPVLYAITAYYVIIFGGRFLLSKSKPFKLN
```

Fig. 25 (continued)

```
          GILTLYNLGITLLSAYMLAELI-----LSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYY
          G:..L:NL :T LS. :L. ::      : . .G Y . C     :.G. .  :..:.:. Y
          GLFQLHNLVLTSLSLTLLLLMVEQLVPIIVQHGLYFAIC----NIGAWTQPLVTLYYMNY

          FSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWCVL------NWIPCGQSFFGPT
          . K :EF:DT.F.VL:.K  ::TFLH.YHH.:.  : :. L      :W:P.       :
          IVKFIEFIDTFFLVLKHK--KLTFLHTYHHGATALLCYTQLMGTTSISWVPI-------S

          LNSFIHILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQFVLTI-----------THTMSA
          LN  :H::MY YY L:   :.   :WWK:::T: Q::QFVL.I           .H.. .
          LNLGVHVVMYWYYFLA---ARGIRVWWKEWVTRFQIIQFVLDIGFIYFAVYQKAVHLYFP

          VVKPCGFPF--------GCLIFQSSYMLTLVILFLNFYVQTYRKKPMK     263
          ::. CG  .        GC.I. SSY:    :LF::FY:..Y::K .K
          ILPHCGDCVGSTTATFAGCAII-SSYL----VLFISFYINVYKRKGTK     305
```

Fig. 26

BLASTP - alignment of 391_protein_modified against swiss|P40319|SUR4_YEAST SUR4 PROTEIN (SRE1 PROTEIN).//:trembl|AF011409|AF011409_1 gene: "VBM1"; product: "v-SNARE bypass mutant gene 1 protein"; Saccharomyces cerevisiae v-SNARE bypass mutant gene 1 protein (VBM1) gene, complete cds. //:trembl|U19103|SCL8039_14 gene: "SUR4"; product: "Sur4p: sterol isomerase"; Saccharomyces cerevisiae chromosome XII cosmid 8039. //:trembl|X82033|SCSRE1_1 gene: "SUR4"; S.cerevisiae SRE1 gene //:trembl|L28723|SCSUR4A_1 gene: "SUR4"; Saccharomyces cerevisiae SUR4 gene, complete cds. //:gp|AF011409|3378048 gene: "VBM1"; product: "v-SNARE bypass mutant gene 1 protein"; Saccharomyces cerevisiae v-SNARE bypass mutant gene 1 protein (VBM1) gene, complete cds. //:gp|X82033|558642 gene: "SUR4"; S.cerevisiae SRE1 gene.
//:gp|U19103|609406 gene: "SUR4"; product: "Sur4p: sterol isomerase"; Saccharomyces cerevisiae chromosome XII cosmid 8039. //:gp|L28723|453568 gene: "SUR4"; Saccharomyces cerevisiae SUR4 gene, complete cds.

This hit is scoring at : 1e-16 (expectation value)
Alignment length (overlap) : 293
Identities : 25 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:      30 FMLDSYLPTFFLTVMYLLSIWLGNKYMK--NRPALSLRGILTLYNLGITLLSAY----ML
           F:.:.Y .. .:.V.Y:: I: G...::  N...L..: :..:NL :T :S..    ML
H:      69 FLANGYHAVSIIIVYYII-IFGGQAILRALNASPLKFKLLFEIHNLFLTSISLVLWLLML
```


Fig. 26 (continued)

```
           AELILSTWEGGYNLQCQDLTSAGEADIRVAKVLWWYYFSKSVEFLDTIFFVLRKKTSQIT
           .:L: ..:..G.     .:.S. .   ::..:.:  Y.:K VE.:DT:F.VLR:K  ::.
           EQLVPMVYHNGL---FWSICSKEAFAPKLVTLYYLNYLTKFVELIDTVFLVLRRK--KLL

           FLHVYHHASMFNIWWCVL------NWIPCGQSFFGPTLNSFIHILMYSYYGLSVFPSMHK
           FLH.YHH.:.  : :. L      .W: .       .LN  :H::MY YY LS   S.
           FLHTYHHGATALLCYTQLIGRTSVEWVVI-------LLNLGVHVIMYWYYFLS---SCGI

           YLWWKKYLTQAQLVQFVLTI------THTMSA------VVKPCGFPFGCLIFQSSYMLTL
            :WWK:::T: Q::QF::.:      T:T. A      ::.  G  :G. . .:  .L.L
           RVWWKQWVTRFQIIQFLIDLVFVYFATYTFYAHKYLDGILPNKGTCYGTQAAAAYGYLIL

      ---VILFLNFYVQTYRKKPMKKDMQEPPAGKEVKNGFSKAYFTAANGVMNKKA      295
         ::LF::FY:Q:Y:K  .K. .:E.... .V.:G S... T: . V.::KA
      TSYLLLFISFYIQSYKKGGKKTVKKESEVSGSVASGSSTGVKTSNTKVSSRKA      345
```

Fig. 27

HMMPFAM - alignment of 391 protein modified against pfam|hmm|GNS1_SUR4
GNS1/SUR4 family -

This hit is scoring at : -31.2 E=4.9e-09
Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```
Q:      5 KAFDDEINAFL--------------DNMFG-----PRDSRVRGWFML-------------
            ... ::.: .                D. F       . .:V  : .
H:      1 aellEkysdLndsssCFLkvfvPsidrPFfnIylwnhfdkvvtystsyrAViFpgeqfef

          ---DSYLPTFFL--------TVMYLLSIWLGNKYMKNR--PALSLRGILTLYNLGITLLS
             .S . .F           .V:Y.: I: G.K.::.    ....L: :L.::NL :T .S
          iqgKSktiLfekylyhaikiivlYyiiIfggqklleklnAKPfkLklllqvhNlfLtsfS

          AY----MLAELILSTWEGG---YNLQCQDLTSAGEAdirvakVLWWY--YFSKSVEFLDT
          ..     M:.:L: S.:. G   Y   C.. . .  .       V. :Y  Y.SK VE.:DT
          llllLlMveqlvpsvyaeGNSLYfsiCnseawtqvl......vtlyylnylsKfvELiDT

          IFFVLRKKtsQITFLHVYHHASMfnIWWCVLNWIPC-GQSFFGPTLNSFIHILMYSYYGL
          :F.VLRK:  ::.FLH.YHH.:.  .  C. . :   . .:.  .LN  :H:LMY YY L
          vFlVLRkR..kLiFLHtYHHgAt..allcyhqlvghTAvgwvpIlLNlgVHvLMYwYYfL

          SvfpSMHKYL--WWKKYLTQAQLVQFVLTIT---HTMSAVVKPCGFP-------------
          S   ::   :  WWK.::T:.Q::QF:L.:.   ..: .      .P
          s...AlGiRvPKWwkmwVTrlQiiQflldvifIyfavYqkkvhkylpgilPncgdCqgsv
```

Fig. 27 (continued)

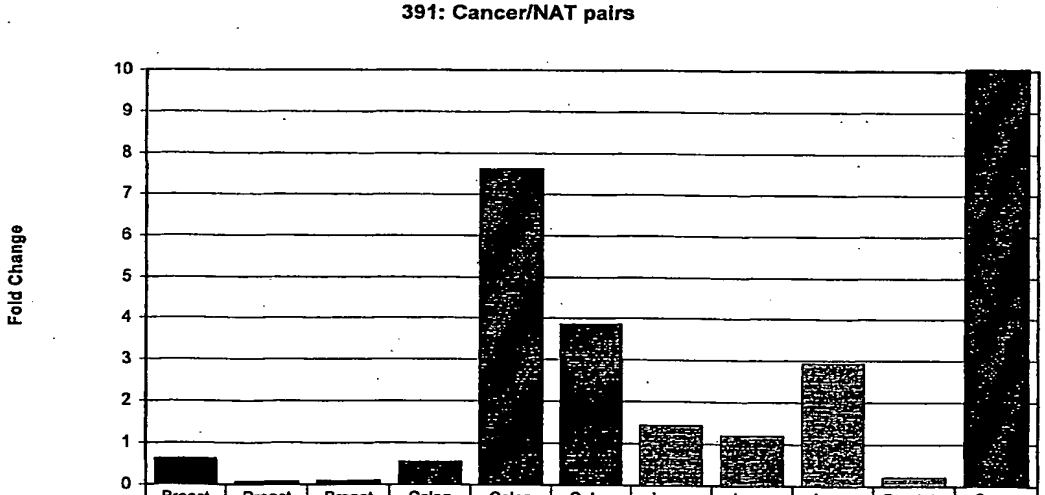
```
          ----FGCLIFqSSYMltlvILFLNFYVQTYRKKPMKKDMQEPPA     271
              .G .I. :SY:    :LF::FY::.Y:KK..K. .: . .
          aalalgfaIl.tsYl....lLFIsFyikaYkkKssktvkkvkne     326
```

Fig. 28

TMHMM result

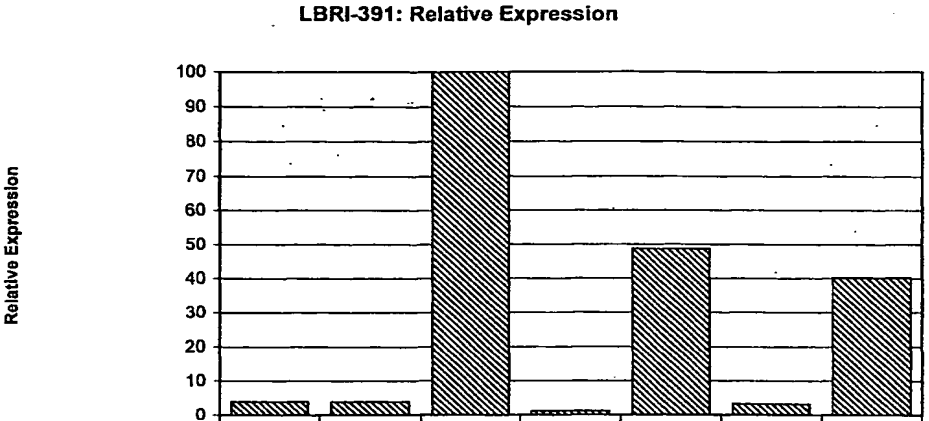
Sequence	TMHMM1.0	outside	1	28
Sequence	TMHMM1.0	TMhelix	29	51
Sequence	TMHMM1.0	inside	52	61
Sequence	TMHMM1.0	TMhelix	62	84
Sequence	TMHMM1.0	outside	85	116
Sequence	TMHMM1.0	TMhelix	117	135
Sequence	TMHMM1.0	inside	136	141
Sequence	TMHMM1.0	TMhelix	142	164
Sequence	TMHMM1.0	outside	165	169
Sequence	TMHMM1.0	TMhelix	170	192
Sequence	TMHMM1.0	inside	193	204
Sequence	TMHMM1.0	TMhelix	205	223
Sequence	TMHMM1.0	outside	224	231
Sequence	TMHMM1.0	TMhelix	232	254
Sequence	TMHMM1.0	inside	255	295

Fig. 29



	Breast Cancer 5781	Breast Cancer 5922	Breast Cancer 5988	Colon Cancer 5255	Colon Cancer 5295	Colon Cancer 5298	Lung Cancer 5299 B	Lung Cancer 5662	Lung Cancer 5833	Prostate CAN 5917	Ovary CAN 6145
Fold Induction	0,63728	0,070805	0,098073	0,552865	7,621104	3,850378	1,428994	1,193336	2,928171	0,210954	73,00888
391-Ct	30,255	35,85	32,61	34,145	32,875	32,645	31,04	34,225	30,705	30,255	27,355
18s-Ct	15,785	16,54	16,53	16,46	16,975	16,51	17,205	18,435	16,03	17,755	18,445

Fig. 30



	adipose mesenteric	adipose subcutaneous	brain	islets	hypothalamus	liver	skeletal muscle
391-Ct	32,745	32,125	27,54	34,66	28,47	32,415	29,005
18s-Ct	15,495	14,855	14,91	15,57	14,8	14,86	15,06
Relative Expression	4,0666933	4,0107059	100	1,135916	48,632747	3,2917532	40,192549

Fig. 31

BLASTP - alignment of 391_protein_modified against tremblnew|AF277094|AF277094_1

product: "ELOVL4"; Homo sapiens ELOVL4 mRNA, complete cds.
//:tremblnew|AF279654|AF279654_1 product: "ELOVL4"; Homo sapiens ELOVL4 gene, exon 6 and complete cds. //:gpnew|AF277094|12044043 product: "ELOVL4"; Homo sapiens ELOVL4 mRNA, complete cds. //:gpnew|AF279654|12044051 product: "ELOVL4"; Homo sapiens
ELOVL4 gene, exon 6 and complete cds.

This hit is scoring at : 1e-71 (expectation value)
Alignment length (overlap) : 276
Identities : 44 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:      23 DSRVRGWFMLDSYLPTFFLTVMYLLSIWLGNKYMKNRPALSLRGILTLYNLGITLLSAYM
           D.RV..W ::.S  PT. ::.:YLL :WLG K:MK:R....:R :L.:YN.G:.LL:.::
H:      34 DKRVENWPLMQSPWPTLSISTLYLLFVWLGPKWMKDREPFQMRLVLIIYNFGMVLLNLFI

           LAELILSTWEGGYNLQCQDLTSAGEA-DIRVAKVLWWYYFSKSVEFLDTIFFVLRKKTSQ
           ..EL.:.::..GY:. CQ.:. :... ::R:A..LWWY:.SK.VE:LDT:FF:LRKK.:Q
           FRELFMGSYNAGYSYICQSVDYSNNVHEVRIAAALWWYFVSKGVEYLDTVFFILRKKNNQ
```

Fig. 31 (continued)

```
ITFLHVYHHASMFNIWWCVLNWIPCGQSFFGPTLNSFIHILMYSYYGLSVF-PSMHKYLW
::FLHVYHH.:MF.:WW. :.W:. GQ:FFG..LNSFIH::MYSYYGL:.F P :.KYLW
VSFLHVYHHCTMFTLWWIGIKWVAGGQAFFGAQLNSFIHVIMYSYYGLTAFGPWIQKYLW

WKKYLTQAQLVQFVLTITHTMSAVVKPCGFPFGCLIFQSSYMLTLVILFLNFYVQTYRKK
WK:YLT..QL:QF :TI HT. ::...C FP  .     :Y.::.:.LFLNFY::TY
WKRYLTMLQLIQFHVTIGHTALSLYTDCPFPKWMHWALIAYAISFIFLFLNFYIRTY---

PMKKDMQEPPAGKEVKNGFSKAYFTAANGVMNKKAQ     296
   K: ::P.AGK...NG.S       ANGV...:.Q
---KEPKKPKAGKTAMNGIS------ANGVSKSEKQ     297
```

SEQUENCE LISTING

<110> Bayer AG

<120> REGULATION OF HUMAN ELONGASE HSELO1-LIKE PROTEIN

<130> LIO280 Foreign Countries

<150> US 60/267,150

<151> 2002-02-08

<150> US 60/331,450

<151> 2002-11-16

<150> US 60/336,164

<151> 2002-12-06

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<170> PatentIn version 3.1

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cttactgtca tgtatctgct ctcaatatgg ctgggtaaca agtatatgaa gaacagacct 180

gctctttctc tcaggggtat cctcaccttg tataatcttg gaatcacact tctctccgcg 240

tacatgctgg cagagctcat tctctccact tgggaaggag gctacaactt acagtgtcaa 300

gatcttacca gcgcagggga agctgacatc cgggtagcca aggtgctttg gtggtactat 360

ttctccaaat cagtagagtt cctggacaca attttcttcg ttttgcggaa aaaaacgagt 420

cagattactt ttcttcatgt atatcatcat gcttctatgt ttaacatctg gtggtgtgtc 480

ttgaactgga taccttgtgg acaaagtttc tttggaccaa cactgaacag ttttgtccac 540

attcttatgt actcctacta tggactttct gtgtttccat ctatgcacaa gtatctttgg 600

tggaagaaat atctcacaca ggctcagctg gtgcagttcg tgctcaccat cacgcacacc 660

atgagcgccg tcgtgaaacc gtgtggcttc cccttcggtt gtctcatctt ccagtcatct 720

tatatgctaa cgttagtcat cctcttctta aatttttatg ttcagacata ccgaaaaaag 780

ccaatgaaga aagatatgca agagccacct gcagggaaag aagtgaagaa tggtttttcc 840

aaagcctact tcactgcagc aaatggagtg atgaacaaga aagcacaata a 891

<210> 2

<211> 296

<212> PRT

<213> Homo sapiens

<400> 2

Met Glu His Leu Lys Ala Phe Asp Asp Glu Ile Asn Ala Phe Leu Asp
1 5 10 15

Asn Met Phe Gly Pro Arg Asp Ser Arg Val Arg Gly Trp Phe Thr Leu
20 25 30

Asp Ser Tyr Leu Pro Thr Phe Phe Leu Thr Val Met Tyr Leu Leu Ser
35 40 45

Ile Trp Leu Gly Asn Lys Tyr Met Lys Asn Arg Pro Ala Leu Ser Leu
50 55 60

Arg Gly Ile Leu Thr Leu Tyr Asn Leu Gly Ile Thr Leu Leu Ser Ala
65 70 75 80

Tyr Met Leu Ala Glu Leu Ile Leu Ser Thr Trp Glu Gly Gly Tyr Asn
85 90 95

Leu Gln Cys Gln Asp Leu Thr Ser Ala Gly Glu Ala Asp Ile Arg Val
100 105 110

Ala Lys Val Leu Trp Trp Tyr Tyr Phe Ser Lys Ser Val Glu Phe Leu
115 120 125

Asp Thr Ile Phe Phe Val Leu Arg Lys Lys Thr Ser Gln Ile Thr Phe
130 135 140

Leu His Val Tyr His His Ala Ser Met Phe Asn Ile Trp Trp Cys Val
145 150 155 160

Leu Asn Trp Ile Pro Cys Gly Gln Ser Phe Phe Gly Pro Thr Leu Asn
165 170 175

Ser Phe Val His Ile Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Val Phe
180 185 190

```
Pro Ser Met His Lys Tyr Leu Trp Trp Lys Lys Tyr Leu Thr Gln Ala
        195                 200                 205

Gln Leu Val Gln Phe Val Leu Thr Ile Thr His Thr Met Ser Ala Val
    210                 215                 220

Val Lys Pro Cys Gly Phe Pro Phe Gly Cys Leu Ile Phe Gln Ser Ser
225                 230                 235                 240

Tyr Met Leu Thr Leu Val Ile Leu Phe Leu Asn Phe Tyr Val Gln Thr
            245                 250                 255

Tyr Arg Lys Lys Pro Met Lys Lys Asp Met Gln Glu Pro Pro Ala Gly
            260                 265                 270

Lys Glu Val Lys Asn Gly Phe Ser Lys Ala Tyr Phe Thr Ala Ala Asn
        275                 280                 285

Gly Val Met Asn Lys Lys Ala Gln
    290                 295
```

<210> 3

<211> 296

<212> PRT

<213> Homo sapiens

<400> 3

```
Met Glu His Leu Lys Ala Phe Asp Asp Glu Ile Asn Ala Phe Leu Asp
1               5                   10                  15

Asn Met Phe Gly Pro Arg Asp Ser Arg Val Arg Gly Trp Phe Thr Leu
            20                  25                  30
```



```
Asp Ser Tyr Leu Pro Thr Phe Phe Leu Thr Val Met Tyr Leu Leu Ser
        35                  40                  45

Ile Trp Leu Gly Asn Lys Tyr Met Lys Asn Arg Pro Ala Leu Ser Leu
    50                  55                  60

Arg Gly Ile Leu Thr Leu Tyr Asn Leu Gly Ile Thr Leu Leu Ser Ala
65                  70                  75                  80

Tyr Met Leu Ala Glu Leu Ile Leu Ser Thr Trp Glu Gly Gly Tyr Asn
                85                  90                  95

Leu Gln Cys Gln Asp Leu Thr Ser Ala Gly Glu Ala Asp Ile Arg Val
            100                 105                 110

Ala Lys Val Leu Trp Trp Tyr Tyr Phe Ser Lys Ser Val Glu Phe Leu
        115                 120                 125

Asp Thr Ile Phe Phe Val Leu Arg Lys Lys Thr Ser Gln Ile Thr Phe
    130                 135                 140

Leu His Val Tyr His His Ala Ser Met Phe Asn Ile Trp Trp Cys Val
145                 150                 155                 160

Leu Asn Trp Ile Pro Cys Gly Gln Ser Phe Phe Gly Pro Thr Leu Asn
                165                 170                 175

Ser Phe Val His Ile Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Val Phe
            180                 185                 190

Pro Ser Met His Lys Tyr Leu Trp Trp Lys Lys Tyr Leu Thr Gln Ala
        195                 200                 205

Gln Leu Val Gln Phe Val Leu Thr Ile Thr His Thr Met Ser Ala Val
    210                 215                 220
```

```
Val Lys Pro Cys Gly Phe Pro Phe Gly Cys Leu Ile Phe Gln Ser Ser
225                 230                 235                 240

Tyr Met Leu Thr Leu Val Ile Leu Phe Leu Asn Phe Tyr Val Gln Thr
                245                 250                 255

Tyr Arg Lys Lys Pro Met Lys Lys Asp Met Gln Glu Pro Pro Ala Gly
            260                 265                 270

Lys Glu Val Lys Asn Gly Phe Ser Lys Ala Tyr Phe Thr Ala Ala Asn
        275                 280                 285

Gly Val Met Asn Lys Lys Ala Gln
    290                 295
```

<210> 4

<211> 296

<212> PRT

<213> Homo sapiens

<400> 4

```
Met Glu His Leu Lys Ala Phe Asp Asp Glu Ile Asn Ala Phe Leu Asp
1               5                   10                  15

Asn Met Phe Gly Pro Arg Asp Ser Arg Val Arg Gly Trp Phe Met Leu
            20                  25                  30

Asp Ser Tyr Leu Pro Thr Phe Phe Leu Thr Val Met Tyr Leu Leu Ser
        35                  40                  45

Ile Trp Leu Gly Asn Lys Tyr Met Lys Asn Arg Pro Ala Leu Ser Leu
    50                  55                  60
```



```
Arg Gly Ile Leu Thr Leu Tyr Asn Leu Gly Ile Thr Leu Leu Ser Ala
65                  70                  75                  80

Tyr Met Leu Ala Glu Leu Ile Leu Ser Thr Trp Glu Gly Gly Tyr Asn
                85                  90                  95

Leu Gln Cys Gln Asp Leu Thr Ser Ala Gly Glu Ala Asp Ile Arg Val
            100                 105                 110

Ala Lys Val Leu Trp Trp Tyr Tyr Phe Ser Lys Ser Val Glu Phe Leu
        115                 120                 125

Asp Thr Ile Phe Phe Val Leu Arg Lys Lys Thr Ser Gln Ile Thr Phe
    130                 135                 140

Leu His Val Tyr His His Ala Ser Met Phe Asn Ile Trp Trp Cys Val
145                 150                 155                 160

Leu Asn Trp Ile Pro Cys Gly Gln Ser Phe Phe Gly Pro Thr Leu Asn
                165                 170                 175

Ser Phe Ile His Ile Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Val Phe
            180                 185                 190

Pro Ser Met His Lys Tyr Leu Trp Trp Lys Lys Tyr Leu Thr Gln Ala
        195                 200                 205

Gln Leu Val Gln Phe Val Leu Thr Ile Thr His Thr Met Ser Ala Val
    210                 215                 220

Val Lys Pro Cys Gly Phe Pro Phe Gly Cys Leu Ile Phe Gln Ser Ser
225                 230                 235                 240

Tyr Met Leu Thr Leu Val Ile Leu Phe Leu Asn Phe Tyr Val Gln Thr
                245                 250                 255
```

Tyr Arg Lys Lys Pro Met Lys Lys Asp Met Gln Glu Pro Pro Ala Gly
260 265 270

Lys Glu Val Lys Asn Gly Phe Ser Lys Ala Tyr Phe Thr Ala Ala Asn
275 280 285

Gly Val Met Asn Lys Lys Ala Gln
290 295

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<210> 6

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 6
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<211> 2340

<212> DNA

<213> Homo sapiens

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<210> 8

<211> 1088

<212> DNA

<213> Homo sapiens

<220>

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ctcttacctt cctacctttt ttcttactgt catgtatctg ctctcaatat ggctgggtaa 240

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tggaatcaca cttctctccg cgtacatgct ggcagagctc attctctcca cttgggaagg 360

aggctacaag cttacagtgt caagatctta ccagcgcagg ggaagctgac atccgggtag 420

ccaaggtgct tcggtggtac tatttctcca aatcagtaga gttcctggac acaatttttct 480

tcgttttgcg gaaaaaaacg agtcagatta cttttcttca tgtatatcat catgcttcta 540

tgtttaacat ctggtggtgt gtcttgaact ggatacctgg tggacaaagt ttctttggac 600

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<210> 9

<211> 435

<212> DNA

<213> Homo sapiens

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acatccgggt agccaaggtg ctttggtggt actatttctc caaatcagta gagttcctgg 180

acacaatttt cttcgttttg cggaaaaaaa cgagtcagat tacttttctt catgtatatc 240

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gtttctttgg accaacactg aacagtttta tccacattct tatgtactcc tactatggac 360

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agctggtgca gttcg 435

<210> 10

<211> 421

<212> DNA

<213> Homo sapiens

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t 421

<210> 11

<211> 397

<212> DNA

<213> Homo sapiens

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ctgtgggagg gagggagaga gaagctgcac cagttctgag gtcctcggag gtgagcatca 180

cctcaatgct gatcaaagca ttcagttaac agattaacct aatagcaata tattaataca 240

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<210> 12

<211> 360

<212> DNA

<213> Homo sapiens

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<223> n = a, t, g, or c

<220>
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<223> n = a, t, g, or c

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<221> misc_feature
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<223> n = a, t, g, or c

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<223> n = a, t, g, or c

<220>
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<222> (118)..(118)
<223> n = a, t, g, or c

<220>
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<222> (248)..(248)
<223> n = a, t, g, or c

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tttacaacaa aatgttaatt atattctaaa tacagggtat gttctaatct atattaagca 180

ataatgccag tgcataatca ttccatttgt tcctttagca atcaacccca gaaaatatta 240

aaatgggntc atacacagaa gatagaaaca tctagcaaaa cttctctttc tgtaagccag 300

agtcttgtct atcagattcc cacaaccact cctgattcta aaatttagtg gatatgggta 360

<210> 13
<211> 238
<212> DNA
<213> Homo sapiens

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<210> 14
<211> 217
<212> DNA
<213> Homo sapiens

<400> 14
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<210> 15

<211> 534

<212> DNA

<213> Homo sapiens

<220>

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<222> (405)..(405)

<223> n = a, t, g, or c

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<223> n = a, t, g, or c

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<223> n = a, t, g, or c

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<223> n = a, t, g, or c

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<210> 16

<211> 435

<212> DNA

<213> Homo sapiens

<400> 16
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gtttctttgg accaacactg aacagtttta tccacattct tatgtactcc tactatggac 360

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<210> 17

<211> 3708

<212> DNA

<213> Homo sapiens

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<210> 18

<211> 299

<212> PRT

<213> Homo sapiens

<400> 18

Met Glu His Phe Asp Ala Ser Leu Ser Thr Tyr Phe Lys Ala Leu Leu
1 5 10 15

Gly Pro Arg Asp Thr Arg Val Lys Gly Trp Phe Leu Leu Asp Asn Tyr
20 25 30

Ile Pro Thr Phe Ile Cys Ser Val Ile Tyr Leu Leu Ile Val Trp Leu
35 40 45

Gly Pro Lys Tyr Met Arg Asn Lys Gln Pro Phe Ser Cys Arg Gly Ile
50 55 60

Leu Val Val Tyr Asn Leu Gly Leu Thr Leu Leu Ser Leu Tyr Met Phe
65 70 75 80

```
Cys Glu Leu Val Thr Gly Val Trp Glu Gly Lys Tyr Asn Phe Phe Cys
                85                  90                  95

Gln Gly Thr Arg Thr Ala Gly Glu Ser Asp Met Lys Ile Ile Arg Val
            100                 105                 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe
        115                 120                 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Val Leu His Val
    130                 135                 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
145                 150                 155                 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe Ile
                165                 170                 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser Met
            180                 185                 190

Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Gly Gln Leu Leu
        195                 200                 205

Gln Phe Val Leu Thr Ile Ile Gln Thr Ser Cys Gly Val Ile Trp Pro
    210                 215                 220

Cys Thr Phe Pro Leu Gly Trp Leu Tyr Phe Gln Ile Gly Tyr Met Ile
225                 230                 235                 240

Ser Leu Ile Ala Leu Phe Thr Asn Phe Tyr Ile Gln Thr Tyr Asn Lys
                245                 250                 255

Lys Gly Ala Ser Arg Arg Lys Asp His Leu Lys Asp His Gln Asn Gly
            260                 265                 270
```



```
Ser Met Ala Ala Val Asn Gly His Thr Asn Ser Phe Ser Pro Leu Glu
        275                 280                 285

Asn Asn Val Lys Pro Arg Lys Leu Arg Lys Asp
    290                 295
```

<210> 19

<211> 347

<212> PRT

<213> Homo sapiens

<400> 19

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Met Asn Ser Leu Val Thr Gln Tyr Ala Ala Pro Leu Phe Glu Arg Tyr
1               5                   10                  15

Pro Gln Leu His Asp Tyr Leu Pro Thr Leu Glu Arg Pro Phe Phe Asn
            20                  25                  30

Ile Ser Leu Trp Glu His Phe Asp Asp Val Val Thr Arg Val Thr Asn
        35                  40                  45

Gly Arg Phe Val Pro Ser Glu Phe Gln Phe Ile Ala Gly Glu Leu Pro
    50                  55                  60

Leu Ser Thr Leu Pro Pro Val Leu Tyr Ala Ile Thr Ala Tyr Tyr Val
65                  70                  75                  80

Ile Ile Phe Gly Gly Arg Phe Leu Leu Ser Lys Ser Lys Pro Phe Lys
                85                  90                  95

Leu Asn Gly Leu Phe Gln Leu His Asn Leu Val Leu Thr Ser Leu Ser
            100                 105                 110
```

```
Leu Thr Leu Leu Leu Leu Met Val Glu Gln Leu Val Pro Ile Ile Val
        115                 120                 125

Gln His Gly Leu Tyr Phe Ala Ile Cys Asn Ile Gly Ala Trp Thr Gln
    130                 135                 140

Pro Leu Val Thr Leu Tyr Tyr Met Asn Tyr Ile Val Lys Phe Ile Glu
145                 150                 155                 160

Phe Ile Asp Thr Phe Phe Leu Val Leu Lys His Lys Lys Leu Thr Phe
                165                 170                 175

Leu His Thr Tyr His His Gly Ala Thr Ala Leu Leu Cys Tyr Thr Gln
            180                 185                 190

Leu Met Gly Thr Thr Ser Ile Ser Trp Val Pro Ile Ser Leu Asn Leu
        195                 200                 205

Gly Val His Val Val Met Tyr Trp Tyr Tyr Phe Leu Ala Ala Arg Gly
    210                 215                 220

Ile Arg Val Trp Trp Lys Glu Trp Val Thr Arg Phe Gln Ile Ile Gln
225                 230                 235                 240

Phe Val Leu Asp Ile Gly Phe Ile Tyr Phe Ala Val Tyr Gln Lys Ala
                245                 250                 255

Val His Leu Tyr Phe Pro Ile Leu Pro His Cys Gly Asp Cys Val Gly
            260                 265                 270

Ser Thr Thr Ala Thr Phe Ala Gly Cys Ala Ile Ile Ser Ser Tyr Leu
        275                 280                 285

Val Leu Phe Ile Ser Phe Tyr Ile Asn Val Tyr Lys Arg Lys Gly Thr
    290                 295                 300
```



```
Lys Thr Ser Arg Val Val Lys Arg Ala His Gly Gly Val Ala Ala Lys
305                 310                 315                 320

Val Asn Glu Tyr Val Asn Val Asp Leu Lys Asn Val Pro Thr Pro Ser
                325                 330                 335

Pro Ser Pro Lys Pro Gln His Arg Arg Lys Arg
            340                 345
```

<210> 20

<211> 345

<212> PRT

<213> *Homo sapiens*

<400> 20

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Met Asn Thr Thr Thr Ser Thr Val Ile Ala Ala Val Ala Asp Gln Phe
1               5                   10                  15

Gln Ser Leu Asn Ser Ser Ser Ser Cys Phe Leu Lys Val His Val Pro
            20                  25                  30

Ser Ile Glu Asn Pro Phe Gly Ile Glu Leu Trp Pro Ile Phe Ser Lys
        35                  40                  45

Val Phe Glu Tyr Phe Ser Gly Tyr Pro Ala Glu Gln Phe Glu Phe Ile
    50                  55                  60

His Asn Lys Thr Phe Leu Ala Asn Gly Tyr His Ala Val Ser Ile Ile
65                  70                  75                  80

Ile Val Tyr Tyr Ile Ile Ile Phe Gly Gly Gln Ala Ile Leu Arg Ala
                85                  90                  95
```

```
Leu Asn Ala Ser Pro Leu Lys Phe Lys Leu Leu Phe Glu Ile His Asn
            100                 105                 110

Leu Phe Leu Thr Ser Ile Ser Leu Val Leu Trp Leu Leu Met Leu Glu
        115                 120                 125

Gln Leu Val Pro Met Val Tyr His Asn Gly Leu Phe Trp Ser Ile Cys
    130                 135                 140

Ser Lys Glu Ala Phe Ala Pro Lys Leu Val Thr Leu Tyr Tyr Leu Asn
145                 150                 155                 160

Tyr Leu Thr Lys Phe Val Glu Leu Ile Asp Thr Val Phe Leu Val Leu
                165                 170                 175

Arg Arg Lys Lys Leu Leu Phe Leu His Thr Tyr His His Gly Ala Thr
            180                 185                 190

Ala Leu Leu Cys Tyr Thr Gln Leu Ile Gly Arg Thr Ser Val Glu Trp
        195                 200                 205

Val Val Ile Leu Leu Asn Leu Gly Val His Val Ile Met Tyr Trp Tyr
    210                 215                 220

Tyr Phe Leu Ser Ser Cys Gly Ile Arg Val Trp Trp Lys Gln Trp Val
225                 230                 235                 240

Thr Arg Phe Gln Ile Ile Gln Phe Leu Ile Asp Leu Val Phe Val Tyr
                245                 250                 255

Phe Ala Thr Tyr Thr Phe Tyr Ala His Lys Tyr Leu Asp Gly Ile Leu
            260                 265                 270

Pro Asn Lys Gly Thr Cys Tyr Gly Thr Gln Ala Ala Ala Ala Tyr Gly
        275                 280                 285
```



```
Tyr Leu Ile Leu Thr Ser Tyr Leu Leu Leu Phe Ile Ser Phe Tyr Ile
    290                 295                 300

Gln Ser Tyr Lys Lys Gly Gly Lys Lys Thr Val Lys Lys Glu Ser Glu
305                 310                 315                 320

Val Ser Gly Ser Val Ala Ser Gly Ser Ser Thr Gly Val Lys Thr Ser
                325                 330                 335

Asn Thr Lys Val Ser Ser Arg Lys Ala
            340                 345
```